

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 18:05:14 ; Search time 173 seconds
(without alignments)

2604.485 Million cell updates/sec

Title: US-09-834-792D-4

Perfect score: 6093

Sequence: 1 MQDVQRRPGSGDAEDRE.....HRGGLDGEQAGQPPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 366760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6093	100.0	1165	4	Aab86162 Human MTR
2	6093	100.0	1165	5	Aam51708 Human TRP
3	6093	100.0	1165	5	Abb83855 Human ltr
4	6093	100.0	1165	7	Adj69344 Human hea
5	6093	100.0	1165	8	Adr48686 Transient
6	6078	99.8	1167	8	Adr87161 Human bet
7	6034	99.0	1179	4	Aab86165 Human MTR
8	5088.5	83.5	1158	4	Aab86164 Mouse MTR
9	5088.5	83.5	1158	5	Abb83854 Mouse ltr
10	5088.5	83.5	1158	8	Adr87163 Mouse bet
11	5080.5	83.4	1158	4	Aab86166 Mouse MTR
12	5073	83.3	1157	5	Aam51707 Mouse TRP
13	5025.5	82.5	1156	8	Adr87165 Rat betat
14	5008.5	82.2	1164	5	Abb83853 Rat L-TRP
15	4534	74.4	872	4	Aab86163 Human MTR
16	2448.5	40.2	1166	5	Abg61907 Prostate
17	2448.5	40.2	1166	7	Adn39240 Cancer/an
18	2448.5	40.2	1166	7	Adn39598 Cancer/an
19	2448.5	40.2	1214	3	Aay95436 Human cal
20	2448.5	40.2	1214	7	Adh62712 Ca activa
21	2448.5	40.2	1214	8	Adr73512 Human TRP
22	2448.5	40.2	1214	8	Adsi2775 Transient
23	2444.5	40.1	1214	5	Aae20283 Human Trp
24	2428	39.8	1127	8	Adl06543 Human tum
25	2412.5	39.6	1129	4	Aab85974 Human TLC

ALIGNMENTS

RESULT 1

AAB86162
ID AAB86162 standard; protein; 1165 AA.

XX AC AAB86162;

XX DT 09-AUG-2001 (first entry)

XX DE Human MTR1 protein containing exon 18 fragment.

XX KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
intracellular calcium ion regulation; hormone; growth factor; apoptosis;
cell growth; cell death; cell differentiation; urogenital disease;
polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
rhabdomyosarcoma.

XX OS Homo sapiens.

XX PN WO200132693-A2.

XX PD 10-MAY-2001.

XX PF 06-NOV-2000; 2000WO-DE003876.

XX PR 04-NOV-1999; 99DE-01053167.

XX PA (UYGU-) UNIV GUTENBERG JOHANNES.

XX PI Prawitt D, Pelletier J, Zabel B;

XX WPI; 2001-316417/33.

XX DR N-PSDB; AAH20574.

XX PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann syndrome and tumors, also related proteins and antibodies.

XX PS Claim 10; Fig 4; 46pp; German.

XX CC This invention describes a novel DNA sequence (i) encoding the MTR1 protein that: (i) has at least one biological activity of a TRP (transient receptor potential) family protein; (ii) is connected with etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the invention have anticancer and developmental activity. MTR1 is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis

Adh51623 Human 186
Adr65995 Human pro
Adr66893 Human pro
Abg72088 Human tra
Aa82018 Human sec
Adg12777 Transient
Asg61852 Prostate
Adh12779 Human TRP
Abm84440 Human dia
Adr43185 Human REM
Aay92944 Human TRP
Aay95439 Human cal
Ab36865 Human put
Abb76459 Human tra
Abb84544 Human lon
Adc47022 Human LTR
Adc77685 Human 222
Adc83633 LTRPC3-re
Adg89102 Human uro
Adc47034 Mouse LTR

CC and cell growth, death and differentiation, and in urogenital diseases,
 CC including polycystic kidney disease. (I) and related ribozymes, antisense
 CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
 CC associated with altered expression of the MTR1 gene or activity of its
 CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
 CC thalidomide and rhabdomyosarcoma. Probes from (I), or Ab, are also
 CC used for diagnosis of such diseases. (I) can also be used for recombinant
 CC production of MTR1 proteins (II) (used for analysis, characterization and
 CC therapy), as tissue or chromosomal markers, for identifying genetic
 CC diseases and related sequences, as primers for genetic fingerprinting, as
 CC source of oligonucleotides for biochips, and to raise anti-protein or
 CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
 CC competitive assays for (II), as tissue markers, for identifying
 CC interacting proteins and in screening for (ant)agonists. This sequence
 CC represents a human MTR1 protein described in the method of the invention
 XX
 SQ Sequence 1165 AA;

Query Match 100.0%; Score 6093; DB 4; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MODVQPRGSGDADREDELGHGGEVNFPGSGKRGKFFVVPVSGVAPSVLFDLLAEW 60
 DB 1 MODVQPRGSGDADREDELGHGGEVNFPGSGKRGKFFVVPVSGVAPSVLFDLLAEW 60
 QY 61 HLPAPNLVSVLGEQEPFAMKSWLRLKRLKGLVKAQSTGAWILTSALRVGLRHVGQAV 120
 DB 61 HLPAPNLVSVLGEQEPFAMKSWLRLKRLKGLVKAQSTGAWILTSALRVGLRHVGQAV 120
 QY 121 RHSLASTSTKRVVAVGASLGRVLRRLLEEAQEDFPVHPEDDGGSGPLCSLDSNL 180
 DB 121 RHSLASTSTKRVVAVGASLGRVLRRLLEEAQEDFPVHPEDDGGSGPLCSLDSNL 180
 QY 181 SHFIVPEPGPGKGLTELRLEKHSIQEAGYGGTGSIEIPVLCVLLVNGDNTLRI 240
 DB 181 SHFIVPEPGPGKGLTELRLEKHSIQEAGYGGTGSIEIPVLCVLLVNGDNTLRI 240
 QY 241 SRAVEQAAFWLLVSGGGIADVLAALVNQPHLLVPKVAEKQKFKFSPKHSWEDIVRWT 300
 DB 241 SRAVEQAAFWLLVSGGGIADVLAALVNQPHLLVPKVAEKQKFKFSPKHSWEDIVRWT 300
 QY 301 KLLQNTSHOHLTYDPEQSGSELDVTILKALVACKSHSQSPQDYDLKLAVADR 360
 DB 301 KLLQNTSHOHLTYDPEQSGSELDVTILKALVACKSHSQSPQDYDLKLAVADR 360
 QY 361 VDIKSEIFNGDVEMKSCDLBEVMDVLSNKPFPVRLFDVNGADVADFLTYGRLOELR 420
 DB 361 VDIKSEIFNGDVEMKSCDLBEVMDVLSNKPFPVRLFDVNGADVADFLTYGRLOELR 420
 QY 421 SVSRKSLFDLLQKQBEARLTLAGLGTQQAEPAPFSLHEVSRVLKDFLQDACRG 480
 DB 421 SVSRKSLFDLLQKQBEARLTLAGLGTQQAEPAPFSLHEVSRVLKDFLQDACRG 480
 QY 481 FYQDGRPDARRAEKPAKPTGOKWLDLNKSENPMRDLFLWAVLQNRHEMATYFWAM 540
 DB 481 FYQDGRPDARRAEKPAKPTGOKWLDLNKSENPMRDLFLWAVLQNRHEMATYFWAM 540
 QY 541 QOEGVAALAAACKILKEMSHLETEAEARATREAKYERLALDLFSECVSNSEARAFALLV 600
 DB 541 QOEGVAALAAACKILKEMSHLETEAEARATREAKYERLALDLFSECVSNSEARAFALLV 600
 QY 601 RNRCSKTTCLHLATEADAKAFPAHDGQVQAFLTRIWWGMAAGTPIRLLLGAPLCPALV 660
 DB 601 RNRCSKTTCLHLATEADAKAFPAHDGQVQAFLTRIWWGMAAGTPIRLLLGAPLCPALV 660
 QY 661 YTNLITFSEAPLRTGLDQLDLSLDTSEKSPVGLQSRVEELVEAPRAQDGRPAVFL 720
 DB 661 YTNLITFSEAPLRTGLDQLDLSLDTSEKSPVGLQSRVEELVEAPRAQDGRPAVFL 720
 QY 721 LTRWRKFWGAPVTFLGNVVMYFAPLFTYVLLVDFRPPQSGPSEVLYFWVFTVL 780
 DB 721 LTRWRKFWGAPVTFLGNVVMYFAPLFTYVLLVDFRPPQSGPSEVLYFWVFTVL 780

QY 781 BEIRQGFTEBTDTHLVKKFTLYVGDNNKNCMDVAIFLPIVGVTCRMLPSAFAEAGRTVLAM 840
 DB 781 BEIRQGFTEBTDTHLVKKFTLYVGDNNKNCMDVAIFLPIVGVTCRMLPSAFAEAGRTVLAM 840
 QY 841 DPMVFTLRLHIHFAIHQQLGPKIIVVERMKDVFPFLFFLSVMLVAYGVTTQALLHPHDG 900
 DB 841 DPMVFTLRLHIHFAIHQQLGPKIIVVERMKDVFPFLFFLSVMLVAYGVTTQALLHPHDG 900
 QY 901 RLEWIFRVLRYRPLQIFGOIPDLDEIDEARVNCSTHPLLEDSPSCPSLYANMLVILLV 960
 DB 901 RLEWIFRVLRYRPLQIFGOIPDLDEIDEARVNCSTHPLLEDSPSCPSLYANMLVILLV 960
 QY 961 TFLVTVNLLNLLIAMFSTYFQVQGNADFMKFORYNLIVEYHERPALAPPFILLSHL 1020
 DB 961 TFLVTVNLLNLLIAMFSTYFQVQGNADFMKFORYNLIVEYHERPALAPPFILLSHL 1020
 QY 1021 SLTLRRVPKKEAEHREHLERDLPDLQKVTWETVQKENFLSKMKRRDRSEGEVLRK 1080
 DB 1021 SLTLRRVPKKEAEHREHLERDLPDLQKVTWETVQKENFLSKMKRRDRSEGEVLRK 1080
 QY 1081 TAHRVDPIAKYLGGLREQEKRICKLESQINYSVSVSVADVLAQGGGPRSSQHCGBGSQ 1140
 DB 1081 TAHRVDPIAKYLGGLREQEKRICKLESQINYSVSVSVADVLAQGGGPRSSQHCGBGSQ 1140
 QY 1141 LVAADHRGGLDGEWQPGAGQPPSDT 1165
 DB 1141 LVAADHRGGLDGEWQPGAGQPPSDT 1165

RESULT 2

AA51708
 ID AA51708 standard; protein; 1165 AA.
 XX
 AC AA51708;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Human TRP8.
 XX
 KW Mouse; human; TRP8; transient receptor potential channel;
 KW taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;
 KW pharmaceutical.
 XX
 OS Homo sapiens.
 XX
 DN WO200179448-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US012608.
 XX
 PR 17-APR-2000; 2000US-0197491P.
 PR 13-APR-2001; 2001US-00834792.
 XX
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX
 PI Margolskee RF, Huang L, Rong M, Max M, Perez CA;
 XX
 DR WPI; 2002-017608/02.
 DR N-PSDB; AA199708.
 XX
 PT A new transient receptor potential channel, designated TRP8, is expressed
 PT in taste receptor cells and associated with perception of bitter and
 PT sweet taste, and is useful to find new flavor enhancers.
 XX
 PS Claim 9; Fig 4; 55pp; English.
 XX
 CC The invention relates to a mouse and human transient receptor potential
 CC channel, TRP8, expressed in taste receptor cells and associated with the
 CC perception of bitter and sweet taste. Modulators of TRP8 are useful as
 CC flavour enhancers in foods, beverages and pharmaceuticals

SQ	Sequence 1165 AA;	
Query Match	100.0%; Score 6093; DB 5; Length 1165;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1165; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MDVQGPSPGDAEDRRLGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFDLLLAEW 60	
DB	1 MDVQGPSPGDAEDRRLGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFDLLLAEW 60	
QY	61 HLPAPNLVSVLGEQPPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRVLARHVGQAV 120	
DB	61 HLPAPNLVSVLGEQPPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRVLARHVGQAV 120	
QY	121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIEEAQEDFPVHYPPDDGSGQPLCSLDSNL 180	
DB	121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIEEAQEDFPVHYPPDDGSGQPLCSLDSNL 180	
QY	181 SHFILLVEPPGPKGDLTELRLEKHSIQAGYGGTGSIEIPVLCLLVNGDPNLTLEI 240	
DB	181 SHFILLVEPPGPKGDLTELRLEKHSIQAGYGGTGSIEIPVLCLLVNGDPNLTLEI 240	
QY	241 SRAVEQAAPWLILVSGGGIADVLAALVNQPHLLVPKVAEKQKPEKPSGHFSEWIDIVRT 300	
DB	241 SRAVEQAAPWLILVSGGGIADVLAALVNQPHLLVPKVAEKQKPEKPSGHFSEWIDIVRT 300	
QY	301 KLLQNTSHQHLITVDFEQQSGSELDVILKALVKACKSHSOEPQDYLDLKLAVANDR 360	
DB	301 KLLQNTSHQHLITVDFEQQSGSELDVILKALVKACKSHSOEPQDYLDLKLAVANDR 360	
QY	361 VDIASEIPNGDVEKSCDLBEVMDALVSNKPEFVRLVDNGADVADFLTYGRLOELYR 420	
DB	361 VDIASEIPNGDVEKSCDLBEVMDALVSNKPEFVRLVDNGADVADFLTYGRLOELYR 420	
QY	421 SVSRKSLFLDLQKQEARLTLAGLTQQAEPAPFSLHVSRLVKDFLODQACRG 480	
DB	421 SVSRKSLFLDLQKQEARLTLAGLTQQAEPAPFSLHVSRLVKDFLODQACRG 480	
QY	481 FYQDGRPGDRAEKGPAKPTGQKWLIDLQKSENPRDPLFLWAVLQNRHEMATYFWAM 540	
DB	481 FYQDGRPGDRAEKGPAKPTGQKWLIDLQKSENPRDPLFLWAVLQNRHEMATYFWAM 540	
QY	541 GQGVAAALAAKILKEMSHLETEAARATREKYLALDLFSECYNSBARAFALIV 600	
DB	541 GQGVAAALAAKILKEMSHLETEAARATREKYLALDLFSECYNSBARAFALIV 600	
QY	601 RNRCSKTTCLHLATEADAKAFFAHDGVQAFILTRIWMGDMAAGTPIRLLAGAFLCPALV 660	
DB	601 RNRCSKTTCLHLATEADAKAFFAHDGVQAFILTRIWMGDMAAGTPIRLLAGAFLCPALV 660	
QY	661 YTNLITFSEAPLRTGLELDLSDTEKSPILYGLQSRVEELVEAPRAQDGRGPRAVFL 720	
DB	661 YTNLITFSEAPLRTGLELDLSDTEKSPILYGLQSRVEELVEAPRAQDGRGPRAVFL 720	
QY	721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTFYLLVDPRPPQPGSPGPEVTLFWVFTVLV 780	
DB	721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTFYLLVDPRPPQPGSPGPEVTLFWVFTVLV 780	
QY	781 EIRIQGFDTDEDTHLVKKFTLYVGDNNKCDMVAIFLIVGVTCTMLPSAFEAGRTVLAM 840	
DB	781 EIRIQGFDTDEDTHLVKKFTLYVGDNNKCDMVAIFLIVGVTCTMLPSAFEAGRTVLAM 840	
QY	841 DMVFTLRLHIFAIHQKLPKIIIVVERMMKVFFFLFSLVWLVAIVGVTQALLPHDQ 900	
DB	841 DMVFTLRLHIFAIHQKLPKIIIVVERMMKVFFFLFSLVWLVAIVGVTQALLPHDQ 900	
QY	901 RLEWIFRVLRYLQIFGQIPLEIDEARVNCSTHPLLEDSPSCPSIYANWLIVILLV 960	
DB	901 RLEWIFRVLRYLQIFGQIPLEIDEARVNCSTHPLLEDSPSCPSIYANWLIVILLV 960	
QY	961 TFLLVNTVLLMNLIIAMFSYTFVQVQGNADMFKQFYNIIVYHERPALAPPFILLSHL 1020	
DB	961 TFLLVNTVLLMNLIIAMFSYTFVQVQGNADMFKQFYNIIVYHERPALAPPFILLSHL 1020	

QY	1021 SLTLRRVFKKEAEHREHLERDLPPDLQKQVVTWETVQENFLSKMEKRRDRSSEVLRK 1080	
DB	1021 SLTLRRVFKKEAEHREHLERDLPPDLQKQVVTWETVQENFLSKMEKRRDRSSEVLRK 1080	
QY	1081 TAHRVDFIAKVLGGLREQEKRICKLESQINVCYSLVSSVADVLQAGGPPSSOHCGECSQ 1140	
DB	1081 TAHRVDFIAKVLGGLREQEKRICKLESQINVCYSLVSSVADVLQAGGPPSSOHCGECSQ 1140	
QY	1141 LVAADHRGGLDGWEQPGAGOPPSSDT 1165	
DB	1141 LVAADHRGGLDGWEQPGAGOPPSSDT 1165	
RESULT 3		
ABB83855		
ID	ABB83855 standard; protein; 1165 AA.	
XX	ABB83855;	
AC	AC	
XX	30-SEP-2002 (first entry)	
DT	DT	
XX	Human ltrpc6 SEQ ID NO 8.	
DE	Human; ltrpc6; taste; cell signalling; TC-ICS; food; pharmaceutical;	
XX	taste cell-specific ion channel subunit.	
KW	Homo sapiens.	
XX	WO200254069-A1.	
OS	11-JUL-2002.	
PN	26-DEC-2001; 2001WO-US049808.	
PD	29-DEC-2000; 2000US-0259379P.	
PF	21-DEC-2001; 2001US-00026188.	
XX	(REGC) UNIV CALIFORNIA.	
XX	Zuker CS, Zhang Y;	
PI	WPI; 2002-583632/62.	
XX	N-PSDB; ABR85736.	
DR	Identifying modulators of taste signaling in taste cells for use in food	
XX	and pharmaceutical industries to customize and regulate taste, by	
PT	determining effect of the compound on a taste cell-specific ion channel	
PT	subunit.	
XX	Claim 1; Page 305; 306pp; English.	
PS	The invention relates to identifying (M1) a compound that modulates taste	
XX	signalling in taste cells, by contacting the compound with a eukaryotic	
CC	host cell or cell membrane which expresses a taste cell-specific ion	
CC	channel subunit (TC-ICS), and determining a functional effect of the	
CC	compound upon a transmembrane ion flux of a predetermined ion,	
CC	identifying a compound that modulates taste signaling in taste cells.	
CC	(M1) is useful for identifying a compound that modulates taste signalling	
CC	in taste cells, for identifying a compound that binds to a taste cell	
CC	specific ion channel subunit and for modulating taste signaling in taste	
CC	cells of a mammal, in particular a human. Modulators identified by (M1)	
CC	are used by the food and pharmaceutical industries to customize taste,	
CC	e.g. as additives to food or medicine so that the food or medicine tastes	
CC	different to the subject who ingests it. Bitter medicines can be made to	
CC	taste less bitter and sweet substance can be enhanced. The modulators are	
CC	useful for pharmacological and genetic modulation of taste signalling	
CC	pathways. The taste modulators can be directly administered to mammalian	
CC	subjects for modulation of taste in vivo. The present sequence is that of	
CC	the predicted human ltrpc6 protein of the invention	
XX	Sequence 1165 AA;	
SQ		


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SQ Sequence 1165 AA;
Query Match 100.0%; Score 6093; DB 7; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDVQGPFGPGDAEDRRLGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFOLLALAEW 60
Db 1 MDVQGPFGPGDAEDRRLGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFOLLALAEW 60
QY 61 HLPAPNLVSVLGESEPPFAMKSWLDVLRKGLVKAQSTGAWILTSALRGLARHVQAV 120
Db 61 HLPAPNLVSVLGESEPPFAMKSWLDVLRKGLVKAQSTGAWILTSALRGLARHVQAV 120
QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIEEAQEDFPVHYPPEDGSGQPLCSLDSNL 180
Db 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIEEAQEDFPVHYPPEDGSGQPLCSLDSNL 180
QY 181 SHFILLVEPPGPGDGLTELRLRLEKHISEQRAGYGGTGSIEIPVLCILLVNGDPNLTLE 240
Db 181 SHFILLVEPPGPGDGLTELRLRLEKHISEQRAGYGGTGSIEIPVLCILLVNGDPNLTLE 240
QY 241 SRAVEQAAPWLILVSGGGIADYLAALVNQPHLLVPKVAEKQPKFKPSKHSWEDIVRWT 300
Db 241 SRAVEQAAPWLILVSGGGIADYLAALVNQPHLLVPKVAEKQPKFKPSKHSWEDIVRWT 300
QY 301 KLLQNTSHQHLLTYDPEQSGSELDVTILKALVKACKSHSQEPQDYLDLKLAVADR 360
Db 301 KLLQNTSHQHLLTYDPEQSGSELDVTILKALVKACKSHSQEPQDYLDLKLAVADR 360
QY 361 VDIASEIFNGDVEWKSDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR 420
Db 361 VDIASEIFNGDVEWKSDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR 420
QY 421 SVSRKSLLDLQKQEEARLTLAGLGTQQAEPAGPAPFSLHVSRLVKDFLODACRG 480
Db 421 SVSRKSLLDLQKQEEARLTLAGLGTQQAEPAGPAPFSLHVSRLVKDFLODACRG 480
QY 481 FYQDGRPGDRAEKGPAKPTGQKWLIDLNKSENPRDLFLWAVLQNRHEMATYFWAM 540
Db 481 FYQDGRPGDRAEKGPAKPTGQKWLIDLNKSENPRDLFLWAVLQNRHEMATYFWAM 540
QY 541 GQGVAAALAAACKILKEMSHLETAARAATREAKYERLALDLFSECYSNSARAFALIV 600
Db 541 GQGVAAALAAACKILKEMSHLETAARAATREAKYERLALDLFSECYSNSARAFALIV 600
QY 601 RNRCSKTTCLHLATEADAKAFPAHDGVQAFILRIWGDMAAGTPIRLLLGAFCLPALV 660
Db 601 RNRCSKTTCLHLATEADAKAFPAHDGVQAFILRIWGDMAAGTPIRLLLGAFCLPALV 660
QY 661 YTNLITFSEAPLRTGLELDLSDTEKSPLYGLQSRVEELVEAPRAQGRGPRAVFL 720
Db 661 YTNLITFSEAPLRTGLELDLSDTEKSPLYGLQSRVEELVEAPRAQGRGPRAVFL 720
QY 721 LTRWRKFWGAPVTFVGNVVMYFAFLFTYVLLVDPRPPQPGSPGPEVTLFWVFTVLV 780
Db 721 LTRWRKFWGAPVTFVGNVVMYFAFLFTYVLLVDPRPPQPGSPGPEVTLFWVFTVLV 780
QY 781 EETRQGFDTDEDTHLVKCKFTLYVGDNNKCDMVAIFLIVGVTCTRMPLSAFAEAGRTVLAM 840
Db 781 EETRQGFDTDEDTHLVKCKFTLYVGDNNKCDMVAIFLIVGVTCTRMPLSAFAEAGRTVLAM 840
QY 841 DMVFTLRLIHPAIHKQLGPKIIVVERMMKOVFFFLFSLVWLVAYGVTTQALLPHDQ 900
Db 841 DMVFTLRLIHPAIHKQLGPKIIVVERMMKOVFFFLFSLVWLVAYGVTTQALLPHDQ 900
QY 901 RLEWIFRRLVRYPLQIFGQIPDEIDEARVNCSTHPLLEDSPSCPSYANWLVILLV 960
Db 901 RLEWIFRRLVRYPLQIFGQIPDEIDEARVNCSTHPLLEDSPSCPSYANWLVILLV 960
QY 961 TELLVNTVLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVYHERPALAPPFILLSHL 1020
Db 961 TELLVNTVLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVYHERPALAPPFILLSHL 1020
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QY 1021 SLTLRRVFKKEAEHREHLERDLDPDLQKVVWTETVQENFNLKMEKRRDRDSEGEVLK 1080
Db 1021 SLTLRRVFKKEAEHREHLERDLDPDLQKVVWTETVQENFNLKMEKRRDRDSEGEVLK 1080
QY 1081 TAHRVDPIAKYGLGLREQEKRIKLESQINVCYSLVSSVADVLQGGGPRSSOHCGGSG 1140
Db 1081 TAHRVDPIAKYGLGLREQEKRIKLESQINVCYSLVSSVADVLQGGGPRSSOHCGGSG 1140
QY 1141 LVAADHRGGLDGEQPGAGOPPST 1165
Db 1141 LVAADHRGGLDGEQPGAGOPPST 1165
RESULT 5
ADR48686
ID ADR48686 standard; protein; 1165 AA.
XX
AC ADR48686;
XX
DT 02-DEC-2004 (first entry)
XX
DE Transient receptor potential melastinin-like channel TRPM5 SEQ ID 2.
XX
KW Immunosuppressive; Cytostatic;
KW Calcium receptor potential melastinin-like channel; TRPM5;
KW Calcium-Activated Nonspecific transmembrane channel;
KW CAN transmembrane channel; ion channel; chromosome 11p15.5;
KW autoimmune disorder; graft versus host disease; cancer; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "Encoded by CNN"
FT Misc-difference 14 /note= "Encoded by NNT"
FT Misc-difference 14 /note= "Encoded by NNT"
XX
PN WO2004076632-A2.
XX
PD 10-SEP-2004.
XX
PF 23-FEB-2004; 2004WO-US005316.
XX
PR 21-FEB-2003; 2003US-0448955P.
XX
PA (QUBB-) QUEENS MEDICAL CENT.
XX
PI Penner R, Fleig A;
XX
DR WPI: 2004-662007/64.
XX
DR N-PSDB; ADR48685.
XX
Screening for agent capable of binding to or modulating expression of
transient receptor potential melastinin-like (TRPM5) polypeptide or
modulating ionic permeability of TRPM5 channel, useful for treating
cancer, autoimmune disease.
XX
Claim 3; Fig 7; 69pp; English.
XX
The present invention relates to a method (M1) for screening for
candidate bioactive agents (A1) which are capable of: binding to
transient receptor potential melastinin-like (TRPM5) polypeptide
(ADR48686); modulating monovalent cationic permeability of channel
comprising TRPM5 polypeptide; and modulating expression of TRPM5 nucleic
acid. The method involves contacting TRPM5 polypeptide, channel or cell
expressing TRPM5 nucleic acid with (A1) and detecting whether (A1) causes
the required effect. TRPM5 is a member of the differentiating Calcium-
Activated Nonspecific (CAN) transmembrane channel polypeptide family and
is activated by a rapid increase in intracellular calcium ion (Ca2+)
levels. The TRPM5 coding sequence (ADR48685) was derived from human
kidney cells, however, TRPM5 is broadly expressed in various mammalian
tissues. The presence of TRPM5 in a variety of tissues indicates a
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Generalised role of the channel as a tool that couples agonist-induced intracellular Ca²⁺ release to electrical activity and subsequent cellular responses. The TRPM5 gene was found to be located on chromosome 11p15.5. The candidate bioactive agents identified by (M1), which can open TRPM5 channels in a variety of cell such as cells of nervous, immune, and muscular systems of vertebrates, are useful for treating diseases, and conditions associated with diseases, or disorders, such as autoimmune or graft versus host diseases, or other related autoimmune disorders. The candidate bioactive agents identified by (M1), which can close TRPM5 channels are useful for treating diseases, conditions associated with diseases, or disorders, such as breast and colon cancer or other forms of cancer.

XX
SQ Sequence 1165 AA;

Query Match 100.0%; Score 6093; DB 8; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQDVQPRGSPGDAEDRELGLHGEVNFSGSGKRGKRVGVGAPSVLFDLILAEW 60
DB 1 MQDVQPRGSPGDAEDRELGLHGEVNFSGSGKRGKRVGVGAPSVLFDLILAEW 60

QY 61 HLPAPNLVSVLGEQPPFAMKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLRHVGQAV 120
DB 61 HLPAPNLVSVLGEQPPFAMKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLRHVGQAV 120

QY 121 RHSLASTSTKRVVAVGASGRVLRHRLIEAQAEDFPVHPEDDGGSGPLCSLDSNL 180
DB 121 RHSLASTSTKRVVAVGASGRVLRHRLIEAQAEDFPVHPEDDGGSGPLCSLDSNL 180

QY 181 SHFILLVEPPGPGDGLTELRLEKHISEQAGVGGTGSIEIPVLCLLVNGDPNTLRI 240
DB 181 SHFILLVEPPGPGDGLTELRLEKHISEQAGVGGTGSIEIPVLCLLVNGDPNTLRI 240

QY 241 SRAVQAAPWLLVSGGGIADVLAAQVNPQPHLLVPKVAEQKPKFPKSHFSEWIDVRWT 300
DB 241 SRAVQAAPWLLVSGGGIADVLAAQVNPQPHLLVPKVAEQKPKFPKSHFSEWIDVRWT 300

QY 301 KLLQNTISHQHLTVYDPEQSGSELDTVILKALVKACKSHSQBPQDYLDELKLAVADR 360
DB 301 KLLQNTISHQHLTVYDPEQSGSELDTVILKALVKACKSHSQBPQDYLDELKLAVADR 360

QY 361 VDIASEIFNGDVWKSVDLSEVMDALVSNKPEFVRLVDNGADVADFLTYGRLELYR 420
DB 361 VDIASEIFNGDVWKSVDLSEVMDALVSNKPEFVRLVDNGADVADFLTYGRLELYR 420

QY 421 SVSRKSLFDLLQKQBEARLTLAGLGTQQAAREPPAGPAPSLHEVSRVLKDFLODACRG 480
DB 421 SVSRKSLFDLLQKQBEARLTLAGLGTQQAAREPPAGPAPSLHEVSRVLKDFLODACRG 480

QY 481 FYQGRPGDRRAEKGPAKRPFGQKWLDDLNQKSENPRDLFLWAVLQNRHEMATYFWAM 540
DB 481 FYQGRPGDRRAEKGPAKRPFGQKWLDDLNQKSENPRDLFLWAVLQNRHEMATYFWAM 540

QY 541 QGEGVAAALAAACKILKEMSHLETAARATREAKYERLALDLFSECYNSSEARAFALLV 600
DB 541 QGEGVAAALAAACKILKEMSHLETAARATREAKYERLALDLFSECYNSSEARAFALLV 600

QY 601 RNRCSKTTTCLHLATADAKAFADHGVQAFRLRIWGDMAAGTPTILRLIGALCPALV 660
DB 601 RNRCSKTTTCLHLATADAKAFADHGVQAFRLRIWGDMAAGTPTILRLIGALCPALV 660

QY 661 YTNLITFSEAPLRTGLDQLDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRPRAVFL 720
DB 661 YTNLITFSEAPLRTGLDQLDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRPRAVFL 720

QY 721 LTRWRKFWGAPVTYVFLGNVVFALFTYVLLVDRPPQSGSEVTLTYFWVFTVLV 780
DB 721 LTRWRKFWGAPVTYVFLGNVVFALFTYVLLVDRPPQSGSEVTLTYFWVFTVLV 780

QY 781 BEIRQGFTEDETHLVKFTLYVGDNNKCDMAVFLFIVGVTCTMLPSAFEAGRTVLAM 840
DB 781 BEIRQGFTEDETHLVKFTLYVGDNNKCDMAVFLFIVGVTCTMLPSAFEAGRTVLAM 840

DB 781 BEIRQGFTEDETHLVKFTLYVGDNNKCDMAVFLFIVGVTCTMLPSAFEAGRTVLAM 840
QY 841 DFMVFTLRLIHFALHKLQGPKEIIVVERMKDVFFLFFLSVWLVAYGVTTQALLHPHDG 900
DB 841 DFMVFTLRLIHFALHKLQGPKEIIVVERMKDVFFLFFLSVWLVAYGVTTQALLHPHDG 900
QY 901 RLEWIFRVLRYRPLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLVANWLVILLV 960
DB 901 RLEWIFRVLRYRPLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLVANWLVILLV 960
QY 961 TFLITVNTVLLMNLIIAMFSYTFQVQGNADMFQRYNLIIVEYHERPALAPPFILLSHL 1020
DB 961 TFLITVNTVLLMNLIIAMFSYTFQVQGNADMFQRYNLIIVEYHERPALAPPFILLSHL 1020
QY 1021 SLTLRRVFKKEAEHREHLERDLDPDLDQKVVTWETVQENFLSKMEKRDRDSEGEVLRK 1080
DB 1021 SLTLRRVFKKEAEHREHLERDLDPDLDQKVVTWETVQENFLSKMEKRDRDSEGEVLRK 1080
QY 1081 TAHRVDPIAKYLGGLRREQEKRIKCLESIQINVCVSVSVADVLAQGGPRSSQHCGEQS 1140
DB 1081 TAHRVDPIAKYLGGLRREQEKRIKCLESIQINVCVSVSVADVLAQGGPRSSQHCGEQS 1140
QY 1141 LVAADHRGGLDGMEOPCAGOPPSSDT 1165
DB 1141 LVAADHRGGLDGMEOPCAGOPPSSDT 1165

RESULT 6
ADDR87161
ID ADDR87161 standard; protein; 1167 AA.
XX ADDR87161;
XX ADDR87161;
DT 02-DEC-2004 (first entry)
XX Human betaTRP amino acid sequence, seq id 2.
DE Antidiabetic; betaTRP modulator; gene therapy; glucose; insulin; betaTRP;
KW beta transducin; diabetes; type 2; human.
XX Homo sapiens.
FH Key Location/Qualifiers
FT Region 734..757
FT /note= "Transmembrane region"
FT Region 771..790
FT /note= "Transmembrane region"
FT Region 809..826
FT /note= "Transmembrane region"
FT Region 838..857
FT /note= "Transmembrane region"
FT Region 875..897
FT /note= "Transmembrane region"
FT Region 957..979
FT /note= "Transmembrane region"
FT Region 994..999
FT /note= "TRP motif"
XX W02004079372-A1.
XX 16-SEP-2004.
XX 04-MAR-2004; 2004WO-US006697.
XX 05-MAR-2003; 2003US-0452596P.
XX (META-) METABOLEX INC.
XX Johnson JD, Zhou Y;
XX WPI; 2004-668668/65.
XX DR N-PSDB; ADDR87160.
XX

identifying agents that induce glucose-stimulated insulin production in an animal, useful for treating diabetes, comprises contacting an agent to a polypeptide and selecting an agent that binds or enhances its expression/activity.

Claim 1; SEQ ID NO 2; 83pp; English.

The invention relates to a method for identifying an agent that induces glucose-stimulated insulin production in an animal. The method comprises contacting an agent to a betatRNP polypeptide, and selecting an agent that binds to it or enhances its expression or activity. Further disclosed is a method for expressing betatRNP (beta-transducin protein) in a pancreatic islet cell. The method is useful for identifying an agent that induces glucose-stimulated insulin production in an animal, and thus treating individuals having Type 2 diabetes mellitus or having a predisposition for it. The current sequence represents the human betatRNP amino acid sequence.

Sequence 1167 AA;

Query Match	99.8%	Score 6078	DB 8	Length 1167
Best Local Similarity	99.7%	Pred. No. 0		
Matches 1164	Conservative 1	Mismatches 0	Indels 2	Gaps 1
Qy	1	MODVQGRPGSGDAEDRRELGLHRGEVNFVGGSGKGRKFVRVPSGVAPSVLFDLLLAEW	60	
Db	1	MODVQGRPGSGDAEDRRELGLHRGEVNFVGGSGKGRKFVRVPSGVAPSVLFDLLLAEW	60	
Qy	61	HLPAPNLVSVLVBGEQPFAMKSWLDRVLKGLVTKAAQSTGAWILTSALRVGLARHVGOAV	120	
Db	61	HLPAPNLVSVLVBGEQPFAMKSWLDRVLKGLVTKAAQSTGAWILTSALRVGLARHVGOAV	120	
Qy	121	RDHSLASTSTKRVVAVVAGMASLGRVHLRRILLEEAO--EDFPVHYPEDDGGSGQPLCSLDS	178	
Db	121	RDHSLASTSTKRVVAVVAGMASLGRVHLRRILLEEAOVHEDFPVHYPEDDGGSGQPLCSLDS	180	
Qy	179	NLSHFILVEPPGPGKDGGLTELRLRLKXHISEORAGYGGTGSIEIPIVLCLLVNGDPNTLE	238	
Db	181	NLSHFILVEPPGPGKDGGLTELRLRLKXHISEORAGYGGTGSIEIPIVLCLLVNGDPNTLE	240	
Qy	239	RISRAVEQAAPWLILVGGGIADVLAAALVNPHILLVPKVAEKQFKEKPSKHFSEDIVR	298	
Db	241	RISRAVEQAAPWLILVGGGIADVLAAALVNPHILLVPKVAEKQFKEKPSKHFSEDIVR	300	
Qy	299	WTKLLQNTTSHQHLITVYDFPEQEGSEELDTVLKALVRACKSHSOEPDYLDLDELKLA	358	
Db	301	WTKLLQNTTSHQHLITVYDFPEQEGSEELDTVLKALVRACKSHSOEPDYLDLDELKLA	360	
Qy	359	DRVDIAKSEIFNGDVEWVSKCDLVEVWVDAVSNKPEFVRLFVDNGADVADFLITYGRLOEL	418	
Db	361	DRVDIAKSEIFNGDVEWVSKCDLVEVWVDAVSNKPEFVRLFVDNGADVADFLITYGRLOEL	420	
Qy	419	YRSVRKSLIFDILLQKQBEARLTLAGLTQQAEPFAGPPAFSLHEVSRVLKDFLQDAC	478	
Db	421	YRSVRKSLIFDILLQKQBEARLTLAGLTQQAEPFAGPPAFSLHEVSRVLKDFLQDAC	480	
Qy	479	RGFYQDGRPGDRRAEKGPAKPTGQKWLDDLNOXSENPRDLFLWAVLQNRHEMATYFW	538	
Db	481	RGFYQDGRPGDRRAEKGPAKPTGQKWLDDLNOXSENPRDLFLWAVLQNRHEMATYFW	540	
Qy	539	AMQGGVAAALAAACKILKEMSHLETAEAAARATREAKYERLALDLFSECYSNSEARAFAL	598	
Db	541	AMQGGVAAALAAACKILKEMSHLETAEAAARATREAKYEQALDLFSECYSNSEARAFAL	600	
Qy	599	LVRRNRCNSKTTCLHLATEADAKAPFAHGVGOAFLTRIWWGDMAAGTPTILRLLAGFLCPA	658	
Db	601	LVRRNRCNSKTTCLHLATEADAKAPFAHGVGOAFLTRIWWGDMAAGTPTILRLLAGFLCPA	660	
Qy	659	LVYTNLTITSEBAPLFTGLIEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRGPRAV	718	
Db	661	LVYTNLTITSEBAPLFTGLIEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRGPRAV	720	
Qy	719	FLLTRWRKFWGAPVTIVFLGNVVMYFAFLFTYTVLLVDFRPPQSGSGEVTLYFWVFTL	778	

CC (transient receptor potential) family protein; (ii) is connected with
 CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
 CC with tumors involving 11p15.5 abnormalities. The products of the
 CC invention have anticancer and developmental activity. MTR1 is involved in
 CC regulation of intracellular calcium ion levels, which are essential for
 CC cellular responses to hormones and/or growth factors; also in apoptosis
 CC and cell growth, death and differentiation, and in urogenital diseases,
 CC including polycystic kidney disease. (I) and related ribozymes, antisense
 CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
 CC associated with altered expression of the MTR1 gene or activity of its
 CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
 CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
 CC used for diagnosis of such diseases. (I) can also be used for recombinant
 CC production of MTR1 proteins (II) (used for analysis, characterization and
 CC therapy), as tissue or chromosomal markers, for identifying genetic
 CC diseases and related sequences, as primers for genetic fingerprinting, as
 CC source of oligonucleotides for biochips, and to raise anti-protein or
 CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
 CC competitive assays for (II), as tissue markers; for identifying
 CC interacting proteins and in screening for (ant)agonists. This sequence
 CC represents a human MTR1 protein described in the method of the invention
 CC
 XX Sequence 1179 AA;

Query Match 99.0%; Score 6034; DB 4; Length 1179;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1162; Conservative 0; Mismatches 2; Indels 16; Gaps 3;
 QY 1 MQDVQCPGSGDADRELGLHRCGEVNFSGGKRGKFRVPSGAPSVLFDLLAEW 60
 DB 1 MQDVQCPGSGDADRELGLHRCGEVNFSGGKRGKFRVPSGAPSVLFDLLAEW 60
 QY 61 HLPAPNLVSLVGEQPFAMKGNLRLDLKGLVKAQAQSTGAMILTSALRVGLRHVGQAV 120
 DB 61 HLPAPNLVSLVGEQPFAMKGNLRLDLKGLVKAQAQSTGAMILTSALRVGLRHVGQAV 120
 QY 121 RHSLASTSTKRVVAVGASLGRVLRHRLLEAEQEDFPVHPEDDGGSGPLCSLSNL 180
 DB 121 RHSLASTSTKRVVAVGASLGRVLRHRLLEAEQEDFPVHPEDDGGSGPLCSLSNL 180
 QY 181 SHFILLVEPGPGKDGTLRLRLKHLSEQAGYGGTSGTIEIPVLCVLLVNGDNTLRI 240
 DB 181 SHFILLVEPGPGKDGTLRLRLKHLSEQAGYGGTSGTIEIPVLCVLLVNGDNTLRI 240
 QY 241 SRAVEQAPWLLVSGGGIADVLAAVQPHLLVPKVAEKQFKGFKPSKFSWEDIVRWT 300
 DB 241 SRAVEQAPWLLVSGGGIADVLAAVQPHLLVPKVAEKQFKGFKPSKFSWEDIVRWT 300
 QY 301 KLLQNTITSHQHLTVYDFEQEGSELDVILKALVKACKSHSQEPQDYDLDELKLVAVDR 360
 DB 301 KLLQNTITSHQHLTVYDFEQEGSELDVILKALVKACKSHSQEPQDYDLDELKLVAVDR 360
 QY 361 VDIKSEIFNGDVEWKSCLBEVMDALVSNKPFVRLFDVNGADVADFTYGRLOLYR 420
 DB 361 VDIKSEIFNGDVEWKSCLBEVMDALVSNKPFVRLFDVNGADVADFTYGRLOLYR 420
 QY 421 SVSRKSLFLDLQKQEARLTLAGLCTQQAAREPPAGPPAPSLHEVSRVLKDFLQACRG 480
 DB 421 SVSRKSLFLDLQKQEARLTLAGLCTQQAAREPPAGPPAPSLHEVSRVLKDFLQACRG 480
 QY 481 FYQGRPGDRRRRKEGPAKRTGQKWLDDLNQSENPNRDLFLWAVLQNRHENAITYFWAM 540
 DB 481 FYQGRPGDRRRRKEGPAKRTGQKWLDDLNQSENPNRDLFLWAVLQNRHENAITYFWAM 540
 QY 541 QGEGVAALAAACKTLKEMSHLETAEAAATREAKYERLAL-----DLFSECYSNSEARA 595
 DB 541 QGEGVAALAAACKTLKEMSHLETAEAAATREAKYERLAL-----DLFSECYSNSEARA 595
 QY 596 FALLVRNRNCSKTTCLHLATEADAKFAFFADGQVQAFLTRIWMGDMAGTPIIRLIGAF 655
 DB 601 FALLVRNRNCSKTTCLHLATE-DAKFAFFADGQVQAFLTRIWMGDMAGTPIIRLIGAF 659
 QY 656 CPALVYTNLITFSEAPLRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQGRGP 715

DB 660 CPALVYTNLITFSEAPLRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQGRGP 719
 QY 716 RAVFLLITWRKFWGAPVTVFIGNVMVPAFLFTFLTYLLVDFRPPPPQSPGPEVTLVFWV 775
 DB 720 RAVFLLITWRKFWGAPVTVFIGNVMVPAFLFTFLTYLLVDFRPPPPQSPGPEVTLVFWV 779
 QY 776 FTLVLEERQCGFFTDDETHLVKKTLLVYGNWNKCDMVAIFLTVGVTCRMLPSAFAGR 835
 DB 780 FTLVLEERQCGFFTDDETHLVKKTLLVYGNWNKCDMVAIFLTVGVTCRMLPSAFAGR 839
 QY 836 TVLWDMFVFTLRILHIFAIHQKLGPKIIIVVERMKDKVFFFLFSLVNLVAYGVTQALL 895
 DB 840 TVLWDMFVFTLRILHIFAIHQKLGPKIIIVVERMKDKVFFFLFSLVNLVAYGVTQALL 899
 QY 896 HPHDGRLEWFRVLYRYPYLIQIQIQLDEIDARVNCSTHPLLEDSPSCPSLYANMLV 955
 DB 900 HPHDGRLEWFRVLYRYPYLIQIQIQLDEIDARVNCSTHPLLEDSPSCPSLYANMLV 959
 QY 956 ILLVTFLLTVNLLNLLIAMFSYTFQVVGQADMPKFORYNLIVEYHERPALAPPI 1015
 DB 960 ILLVTFLLTVNLLNLLIAMFSYTFQVVGQADMPKFORYNLIVEYHERPALAPPI 1019
 QY 1016 LLSHLSLTLRVPKKEA-----EHKREHLERDLPDLPDQKVVTWETVQENFLSK 1065
 DB 1020 LLSHLSLTLRVPKKEA-----EHKREHLERDLPDLPDQKVVTWETVQENFLSK 1079
 QY 1066 MEKRRRDESEGEVLKRTAHRVDFIAKYLGLLREOEKRIKLESQINYSVLVSSVADVLAQ 1125
 DB 1080 MEKRRRDESEGEVLKRTAHRVDFIAKYLGLLREOEKRIKLESQINYSVLVSSVADVLAQ 1139
 QY 1126 GGGPRSSQHCQEGSQLVAADHRGGLDGEQPGAGQPPSDT 1165
 DB 1140 GGGPRSSQHCQEGSQLVAADHRGGLDGEQPGAGQPPSDT 1179
 RESULT 8
 AAB86164
 ID AAB86164 standard; protein; 1158 AA.
 XX AAB86164;
 AC AAB86164;
 XX AAB86164;
 DT 09-AUG-2001 (first entry)
 XX Mouse MTR1 protein.
 DE Mouse MTR1 protein.
 XX MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
 KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
 KW 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
 KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;
 KW cell growth; cell death; cell differentiation; urogenital disease;
 KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
 KW rhabdomyosarcoma.
 XX Mus sp.
 OS Mus sp.
 XX WO200132693-A2.
 PN WO200132693-A2.
 XX 10-MAY-2001.
 PD 10-MAY-2001.
 XX 06-NOV-2000; 2000WO-DE003876.
 PF 06-NOV-2000; 2000WO-DE003876.
 XX 04-NOV-1999; 99DE-01053167.
 PR 04-NOV-1999; 99DE-01053167.
 XX (UYGU-) UNIV GUTENBERG JOHANNES.
 PA (UYGU-) UNIV GUTENBERG JOHANNES.
 XX Prawitt D, Pelletier J, Zabel B;
 PI Prawitt D, Pelletier J, Zabel B;
 XX WPI; 2001-316417/33.
 DR WPI; 2001-316417/33.
 DR N-PSDB; AAH20623.
 XX DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
 PT syndrome and tumors, also related proteins and antibodies.

and pharmaceutical industries to customize and regulate taste, by determining effect of the compound on a taste cell-specific ion channel subunit.

Claim 1; Page 211; 306pp; English.

The invention relates to identifying (M1) a compound that modulates taste signalling in taste cells, by contacting the compound with a eukaryotic host cell or cell membrane which expresses a taste cell-specific ion channel subunit (TC-ICS), and determining a functional effect of the compound upon a transmembrane ion flux of a predetermined ion, identifying a compound that modulates taste signalling in taste cells. (M1) is useful for identifying a compound that modulates taste signalling in taste cells, for identifying a compound that binds to a taste cell specific ion channel subunit and for modulating taste signalling in taste cells of a mammal, in particular a human. Modulators identified by (M1) are used by the food and pharmaceutical industries to customize taste, e.g. as additives to food or medicine so that the food or medicine tastes taste less bitter and sweet substance can be enhanced. The modulators are useful for pharmacological and genetic modulation of taste signalling pathways. The taste modulators can be directly administered to mammalian subjects for modulation of taste in vivo. The present sequence is that of the predicted mouse ltrp5 protein of the invention

Sequence 1158 AA;

Query Match 83.5%; Score 5088.5; DB 5; Length 1158;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

1 MQDVQPRPGSDADRELGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFDLLAEW 60
1 MQTQSCGPPDTEGMEPILCRGEINFGSGKRGKFRVPSGVAPSVLFDLLAEW 60
61 HLPAPNLVSLVGEQEPFAKMSLRLDLKGLVKAQSTGAWILTSALRVGLRHVGQAV 120
61 HLPAPNLVSLVGEQEPFAKMSLRLDLKGLVKAQSTGAWILTSALRVGLRHVGQAV 120
121 RDHSLASTTKRVAVAGMASLGRVLRHRL -EAQDFPVHYDEDDGGSGPLCSLDS 178
121 RDHSLASTTKRVAVAGMASLGRVLRHRL -EAQDFPVHYDEDDGGSGPLCSLDS 178
179 NLSHFLVSPGPGKG-DGLTELRLEKHISEQAGAGGTGTSBIPVLCVLLVNGDNTL 237
181 NLSHFLVSPGPGKG-DGLTELRLEKHISEQAGAGGTGTSBIPVLCVLLVNGDNTL 240
238 ERISRAVEQAAPWLLVGGGGIADVLAALVNPQHLVLPKVAEKQKFKPSKHSWEDIV 297
241 ERISRAVEQAAPWLLVGGGGIADVLAALVNPQHLVLPKVAEKQKFKPSKHSWEDIV 300
298 RWTLLQNTTSHOHLTVYDFEQSGSELDVTILKALVKACKSHSQBPQDYLDLKLAVA 357
301 HWTLLQNTTSHOHLTVYDFEQSGSELDVTILKALVKACKSHSQBPQDYLDLKLAVA 360
358 WDRVDIAKSEIFNGDVEWKSCDLEVMVDALVSNKPFVRLFDVNGADVADFLTYGELQF 417
361 WDRVDIAKSEIFNGDVEWKSCDLEVMVDALVSNKPFVRLFDVNGADVADFLTYGELQF 420
418 LYRSVRSKSLFDLLQKQKQEARLTLAGLQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 477
421 LYHSVSPKSLFELLQKQ 480
478 CRGFYQDQRRRAEKGPAPKPTGOKWLLDLNOKSENPRDLFLWAVLONRHEMATYP 537
481 CRGFYQDQ---RRMEERGPKRPAGQKWLFDLSKSEDPWRDLFLWAVLONRHEMATYP 536
538 WAMQEGVAAALAAACKILKEMSHLETAEEAARATREAKYERLALDFSECYSNSEARAPA 597
537 WAMQEGVAAALAAACKILKEMSHLETAEEAARATREAKYERLALDFSECYSNSEARAPA 596
598 LLVRNRCWSKTTTCLHLATADAKAFPAHDGVAQLTRVWGDMAAGTPIRLLAGFICP 657

Db 597 LLVRNRCWSKTTTCLHLATADAKAFPAHDGVAQLTRVWGDMAAGTPIRLLAGFICP 656
QY 658 ALVYNTLTFSEAPLRTGLEDLQDLSDLTEKSPLYGLOSRLVEELVEAPRAQDGRPRA 717
Db 657 ALIYNTLISFSEDAPQRMDELDLQEPDSDLMKESFLCSRGQLEKLTAPRAPDGLQQA 716
QY 718 VFLTRWKFAGAPVTVFLGNVVMYFAFLFTVTLVDRPPPPQSGSGSEVTLVFWVFT 777
Db 717 AFLTRWKFAGAPVTVFLGNVVMYFAFLFTVTLVDRPPPPQSGSGSEVTLVFWVFT 776
QY 778 LVLBEIRGPTDDBDTHLVKFKFTLYVGDNNKCDMAIFLFIYGVTCRMLPSAFEAGRTV 837
Db 777 LVLBEIRGPTDDBDTHLVKFKFTLYVGDNNKCDMAIFLFIYGVTCRMLPSAFEAGRTV 836
QY 838 LAMPDMFTLRLHIFAIHKOLGPKIIVVERMKDVFFFLFSVMLVAYGVTTQALLHP 897
Db 837 LAIDFMFTLRLHIFAIHKOLGPKIIVVERMKDVFFFLFSVMLVAYGVTTQALLHP 896
QY 898 HDGRLEWIFRRVLRYPYQIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANMLVIL 957
Db 897 HDGRLEWIFRRVLRYPYQIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANMLVIL 956
QY 958 LLVTFELAVTNVLLNLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPPFILL 1017
Db 957 LLVTFELAVTNVLLNLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPPFILL 1016
QY 1018 SHLSLTLRRVFKKEABHKREHLERDLPDLDOKVVTWETVOKENFLSKMEKRRRDESEGV 1077
Db 1017 SHLSLTLRRVFKKEABHKREHLERDLPDLDOKVVTWETVOKENFLSKMEKRRRDESEGV 1076
QY 1078 LRKTAHRVDIAKYIAGLREQKRIKCLSEQYINCSLVSSVADVLAQGGGPRSSQHCCE 1137
Db 1077 LRKTAHRVDIAKYIAGLREQKRIKCLSEQYINCSLVSSVADVLAQGGGPRSSQHCCE 1136
QY 1138 GSQLVAAADHRGGLDGWEQFGAGQPPSDT 1165
Db 1137 RSQPASAREVYLE-----SGLPPSDT 1158
RESULT 10
ID ADR87163
XX ADR87163 standard; protein; 1158 AA.
AC ADR87163;
DT 02-DEC-2004 (first entry)
XX Mouse betaTRP amino acid sequence, seq id 4.
DE Antidiabetic; betaTRP modulator; gene therapy; glucose; insulin; betaTRP;
KW beta transducin; diabetes; type 2; mouse.
XX Mus sp.
XX WO2004079372-A1.
XX 16-SEP-2004.
XX 04-MAR-2004; 2004WO-US0006697.
XX 05-MAR-2003; 2003US-0452596P.
XX (META-) METABOLEX INC.
XX Johnson JD, Zhou Y;
XX WPI; 2004-668668/65.
XX N-FSDS; ADR87162.
DR Identifying agents that induce glucose-stimulated insulin production in
DR an animal, useful for treating diabetes, comprises contacting an agent to
PT a polypeptide and selecting an agent that binds or enhances its
PT expression/activity.

XX PS Disclosure; SEQ ID NO 4; 83pp; English.

XX CC The invention relates to a method for identifying an agent that induces

CC glucose-stimulated insulin production in an animal. The method comprises

CC contacting an agent to a betaTRP polypeptide, and selecting an agent that

CC binds to it or enhances its expression or activity. Further disclosed is

CC a method for expressing betaTRP (beta-transducin protein) in a pancreatic

CC islet cell. The method is useful for identifying an agent that induces

CC glucose-stimulated insulin production in an animal, and thus treating

CC individuals having type 2 diabetes mellitus or having a predisposition

CC for it. The current sequence represents the mouse betaTRP amino acid

XX sequence. 1158 AA;

XX QY Query Match 83.5%; Score 5088.5; DB 8; Length 1158;

XX PS Best Local Similarity 84.1%; Pred. No. 0;

XX CC Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

XX QY 1 MQDVQPRGSGDAEDRELCRLHGEVNFSGGKRGKGFVPSGAPSVLFDLLAEW 60

XX DB 1 MQTQSSCFSPDDEGMEPLCRGEINFGSGKRGKGFVPSGAPSVLFEILLTEW 60

XX QY 61 HLPAPNLVSVLGEERPLANKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGQAV 120

XX DB 61 HLPAPNLVSVLGEERPLANKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGQAV 120

XX QY 121 RDHSLASTSKVRVAVGASLGRVLRHRLRLE- EAQEDFPVHYVEDDGGSGPLCSLDS 178

XX DB 121 RDHSLASTSKVRVAVGASLGRVLRHRLRLE- EAQEDFPVHYVEDDGGSGPLCSLDS 178

XX QY 179 NLSHFILVEPPGKGG- DGLTELRLRLKXHSIORAGYCGTGSIEIPVLCILVNGDNTL 237

XX DB 181 NLSHFILVSGALSGNDGLTELQSLKXHSIORAGYCGTGSIEIPVLCILVNGDNTL 240

XX QY 238 ERISRAVEGAAPWLLVSGGGADVLAALVNPHLLVPKVAEKQKFKPPSHFWSMEDIV 297

XX DB 241 ERISRAVEGAAPWLLVSGGGADVLAALVNPHLLVPKVAEKQKFKPPSHFWSMEDIV 300

XX QY 298 RWTKLQNTSHQHLTVYDFQEGSEELDTVLKALVRACKSHSQEPQDYDELKLAVA 357

XX DB 301 HWTCELLQNTAAPHLLTVYDFQEGSEELDTVLKALVRACKSHSQEPQDYDELKLAVA 360

XX QY 358 WRVDIAKSEIFNGDVEWKSCLLEEVNVDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 417

XX DB 361 WRVDIAKSEIFNGDVEWKSCLLEEVNVDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 420

XX QY 418 LYRSVSRKSLPDLLOKOEAEARLTLAGLTQQAEPAPGAPFSLHEVSRVLKDFLODA 477

XX DB 421 LYHSVSPKSLPDLLOKOEAEARLTLAGLTQQAEPAPGAPFSLHEVSRVLKDFLODA 480

XX QY 478 CRGFYQDGRPGDRRAEKGPAKPTQCKWLLDLNOKSENPRDLFLWAVLQNRHEMATYF 537

XX DB 481 CRGFYQDGRPGDRRAEKGPAKPTQCKWLLDLNOKSENPRDLFLWAVLQNRHEMATYF 536

XX QY 538 WAMQEGVGAALAAKIKEMSHLETAEAEATREAKYERLALDLFSECYNSSEARAF 597

XX DB 537 WAMQEGVGAALAAKIKEMSHLETAEAEATREAKYERLALDLFSECYNSSEARAF 596

XX QY 598 LLVRRNRCSKTTCLHLATADAKAFPAHGVQAFILTRIWGDMAGTPIRLLLGAPLCP 657

XX DB 597 LLVRRNRCSKTTCLHLATADAKAFPAHGVQAFILTRIWGDMAGTPIRLLLGAPLCP 656

XX QY 658 ALVYTNLITFSEBAPLRTGLDQLDLSLDEKSPGLYGLQSRVEELVEAPRAQDRGPR 717

XX DB 657 ALVYTNLITFSEBAPLRTGLDQLDLSLDEKSPGLYGLQSRVEELVEAPRAQDRGPR 716

XX QY 718 VFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTVLLVDRPPPPQSGSEVTLTFWVFT 777

XX DB 717 AFLTLTRWRKFWGAPVTVFLGNVVMYFAFLFTVLLVDRPPPPQSGSEVTLTFWVFT 776

XX QY 778 LVLEERIQGFTEDETHLVKFTLYVEDNWNKCDMVAIFLIVGVTCTRMVPSFEAGRTV 837

XX DB 777 LVLEERIQGFTEDETHLVKFTLYVEDNWNKCDMVAIFLIVGVTCTRMVPSFEAGRTV 836

XX QY 838 LAMDFMFTLRLIHI PAHKQLGPKIIIVVERMKDVEFFLFFSLVWLVAYGVTTQALLHP 897

XX DB 837 LAMDFMFTLRLIHI PAHKQLGPKIIIVVERMKDVEFFLFFSLVWLVAYGVTTQALLHP 896

XX QY 898 HDGRLEWIFRVLRYRPLQIFGQIPDLDEIDEARVNCSTHPLLLDESDSPSLYANWLVL 957

XX DB 897 HDGRLEWIFRVLRYRPLQIFGQIPDLDEIDEARVNCSTHPLLLDESDSPSLYANWLVL 956

XX QY 958 LLVTFLLVTNVLNMLLIAMPSYTFQVQGNADMFQFQRYNLIVEHERPALAPPFLL 1017

XX DB 957 LLVTFLLVTNVLNMLLIAMPSYTFQVQGNADMFQFQRYNLIVEHERPALAPPFLL 1016

XX QY 1018 SHLSILTRRVKPEAEHKEHLERDLPDLPDQKVVVTWETVQENFLSKMEKRRDRDSEGV 1077

XX DB 1017 SHLSILTRRVKPEAEHKEHLERDLPDLPDQKVVVTWETVQENFLSKMEKRRDRDSEGV 1076

XX QY 1078 LRKTAHRVDFIATKYLGLREQEKIKCLESQINYSVSVADVLAQGGPRSSQHCGE 1137

XX DB 1077 LRKTAHRVDFIATKYLGLREQEKIKCLESQINYSVSVADVLAQGGPRSSQHCGE 1136

XX QY 1138 GSQVLAADHRCGLDGEQPGAGQPPSDT 1165

XX DB 1137 RSQPASARDREYLE-----SGLPPSDT 1158

XX RESULT 11

XX AAB86166

XX ID AAB86166 standard; protein; 1158 AA.

XX AC AAB86166;

XX DT 09-AUG-2001 (first entry)

XX DE Mouse MTR1 protein #2.

XX KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;

XX KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;

XX KW lip15.5 abnormality; chromosome 11; anticancer; developmental activity;

XX KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;

XX KW cell growth; cell death; cell differentiation; urogenital disease;

XX KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;

XX KW rhabdomyosarcoma.

XX OS Mus sp.

XX PN WO200132693-A2.

XX PD 10-MAY-2001.

XX PF 06-NOV-2000; 2000WO-DE003876.

XX PR 04-NOV-1999; 99DE-01053167.

XX PA (UYGU-) UNIV GUTENBERG JOHANNES.

XX PI Prawditt D, Pelletier J, Zabel B;

XX PS WPI; 2001-316417/33.

XX PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann

XX PT syndrome and tumors, also related proteins and antibodies.

XX PS Disclosure; Fig 12; 46pp; German.

XX CC This invention describes a novel DNA sequence (I) encoding the MTR1

XX CC protein that: (i) has at least one biological activity of a TRP

XX CC (transient receptor potential) family protein; (ii) is connected with

XX CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected

XX CC with tumors involving lip15.5 abnormalities. The products of the

XX CC invention have anticancer and developmental activity. MTR1 is involved in

regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis and cell growth, death and differentiation, and in urogenital diseases, including polycystic kidney disease. (I) and related ribozymes, antigense RNA, proteins and antibodies (Ab) are used to treat or prevent diseases associated with altered expression of the MTR1 gene or activity of its protein, or with calcium influx into cells, e.g. BWS, Wilms tumor, thabodoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also used for diagnosis of such diseases. (I) can also be used for recombinant production of MTR1 proteins (II) (used for analysis, characterization and therapy), as tissue or chromosomal markers, for identifying genetic diseases and related sequences, as primers for genetic fingerprinting, as source of oligonucleotides for biochips, and to raise anti-protein or anti-DNA antibodies. (II) are used to raise Ab, as reagents in competitive assays for (I), as tissue markers, for identifying interacting proteins and in screening for (ant)agonists. This sequence represents the murine MTR1 gene described in the method of the invention

Sequence 1158 AA;

Db	717	AFLLRMRKFGAPVTVFLGNVVMYFAFLFLTYYLLVDRPPQPGSGSEVTIYFWVFT	776
Qy	778	LVLBEIRQGFDTDETHLVKFTLYVGNWNKCDMAIFLFI VGTVCRLMPSAEAGRTV	837
Db	777	LVLBEIRQGFDTDETHLVKFTLYVEDNWNKCDMAIFLFI VGTVCRLMPSAEAGRTV	836
Qy	838	LAMDPMVFTLRLIHFIAHKQLGPKIIIVBERMKDVFFLFFLSVMLVAYGVTTQALLHP	897
Db	837	LAIDPMVFTLRLIHFIAHKQLGPKIIIVBERMKDVFFLFFLSVMLVAYGVTTQALLHP	896
Qy	898	HGDRLEWIFRVLVRYPLQIFGQIPLDEIDBARVNCSTHPLLEDSPCSLYANMLVIL	957
Db	897	HGDRLEWIFRVLVRYPLQIFGQIPLDEIDBARVNCSTHPLLEDSPCSLYANMLVIL	956
Qy	958	LLVTFLLVTVNLLMNLIIAMFSYTFVQVQGNADMFWKFORNYLIVEYHBPALAPPPILL	1017
Db	957	LLVTFLLVTVNLLMNLIIAMFSYTFVQVQGNADMFWKFORNYLIVEYHBPALAPPPILL	1016
Qy	1018	SHLSILTLRRVFKBAEAKRHELRDLDPDLQDKVVTWETVOKENFSLKMEKRDRDSEGV	1077
Db	1017	SHLSVLKQVFRKEAQHRLERDLDPDLQDKIITWETVOKENFSLMEKRDRDSEGV	1076
Qy	1078	LRTAHRVDFIAKYLGLGRBQEKRIKLESQINYCSVLVSSVADVLAAQGGPRSSQHCGE	1137
Db	1077	LRTAHRVDLIAKYIGGLRQBQEKRIKLESQANYCMLLSSMTDTLAPGGTYSSSQNCGC	1136
Qy	1138	GSQLVAAHRGGLDGWEPQAGQPPSDT	1165
Db	1137	RSQPASARDREYLE-----SGLPSPSDT	1158

PT A new transient receptor potential channel, designated TRP8, is expressed
PT in taste receptor cells and associated with perception of bitter and
PT sweet taste, and is useful to find new flavor enhancers.
XX
PS Claim 8; Fig 2; 55pb; English.

XX The invention relates to a mouse and human transient receptor potential
CC channel, TRP8, expressed in taste receptor cells and associated with the
CC perception of bitter and sweet taste. Modulators of TRP8 are useful as
CC flavour enhancers in foods, beverages and pharmaceuticals
XX
SQ Sequence 1157 AA;
Query Match 83.3%; Score 5073; DB 5; Length 1157;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 981; Conservative 67; Mismatches 106; Indels 14; Gaps 5;
Qy 1 MDVQGPSPGDAEDRRLGLHGEVNFVGGSGKRGKFRVPVSGVAPSVLFDLLAEW 60
Db 1 MOTTQSSCGFPPTDGEWELCRGEINFGSGKRGKFKVVPSSVAPSVLFDLLAEW 60
Qy 61 HLPAPNLVSVLGEQPPAMKSWLRLVRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120
Db 61 HLPAPNLVSVLGEQPPAMKSWLRLVRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120
Qy 121 RDHSLASTSTKRVVAVGASLGRVLRHRIIE--EAQEDFPVHYPEDDGGSGPLCSLDS 178
Db 121 RDHSLASTSTKRVVAVGASLGRVLRHRIIE--EAQEDFPVHYPEDDGGSGPLCSLDS 178
Qy 179 NLSHFILVEPGPPGKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPVLCILLVNGDPNTL 237
Db 181 NLSHFILVESGALSGNDGLTELQSLKHSIQQTGTYGTSCTIQIPVLCILLVNGDPNTL 240
Qy 238 ERISRAVEQAAPWLVGSGGIADVLAALVNPVPHLLVPKVAEKPKKFPSPKHSFEDIV 297
Db 241 ERISRAVEQAAPWLVGSGGIADVLAALVNPVPHLLVPKVAEKPKKFPSPKHSFEDIV 297
Qy 298 RWTLLQNTSHQHLITVDFPQESGSELDVILKALVKAQKSHSQEPQDYLDELKAVA 357
Db 301 HMTLLQNTSHQHLITVDFPQESGSELDVILKALVKAQKSHSQEPQDYLDELKAVA 360
Qy 358 WDRVDIAKSEIENGDEWKSCLDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOE 417
Db 361 WDRVDIAKSEIENGDEWKSCLDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOE 420
Qy 418 LYRSVSRKSLFLDLQKQKOEALTLAAGLTOQAREPPAGPPAFSLHVSRYLKDPLQDA 477
Db 421 LYHSVSPKSLFELLQKHEEGRLTLAAGLTOQAREPPAGPPAFSLHVSRYLKDPLQDA 479
Qy 478 CRGFYQDGPDRRAEKAPKAPRTGQKWLIDLNKSENWPRDLFLWAVLQNRHEMATYF 537
Db 480 CRGFYQDGPDRRAEKAPKAPRTGQKWLIDLNKSENWPRDLFLWAVLQNRHEMATYF 535
Qy 538 WAMQEGVAAALAAACKILKEMSHLEAEARATREAKYERLALDLFSECYNSSEARAPA 597
Db 536 WAMQEGVAAALAAACKILKEMSHLEAEARATREAKYERLALDLFSECYNSSEARAPA 595
Qy 598 LLVRRNRKSKTCLHLATEADAKAFHAGDGVQAFTRIWWGDMAGTPIRLLLGAFCLCP 657
Db 596 LLVRRNRKSKTCLHLATEADAKAFHAGDGVQAFTRIWWGDMAGTPIRLLLGAFCLCP 655
Qy 658 ALVYTNLTTFSEAPLRTGLELDLQDLSLDEKSPYGLQSRVEELVLEAPRAGDGRPPA 717
Db 656 ALVYTNLTTFSEAPLRTGLELDLQDLSLDEKSPYGLQSRVEELVLEAPRAGDGRPPA 715
Qy 718 VELLTTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPGSPGSEVTLTFWVFT 777
Db 716 AFLTTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPGSPGSEVTLTFWVFT 775
Qy 778 LVLEERIQGFPTDTHLVKFTLYYGDNNKCDMVAIFLIVGVTCRMLPSAFAGRTV 837
Db 776 LVLEERIQGFPTDTHLVKFTLYYGDNNKCDMVAIFLIVGVTCRMLPSAFAGRTV 835
Qy 838 LAMDFWVFTLRLIHFALHKLQKPKIIVVERMMKDVFFFLFVSVLVAVGVTTQALLHP 897
Db 836 LAIDFWVFTLRLIHFALHKLQKPKIIVVERMMKDVFFFLFVSVLVAVGVTTQALLHP 895
Qy 898 HDGRLEWIFRRVLYRPLQIFGQIPDEIDEARVNCSTHPLLEDSPSCPSLVANLVIL 957

Db 896 HDGRLEWIFRRVLYRPLQIFGQIPDEIDEARVNCSTHPLLEDSPSCPSLVANLVIL 955
Qy 958 LLVTELLAVTNVLLMNLIIAMFSYTFVQVQGNADMFVKFQRYNLIYVHERPALAPPFILL 1017
Db 956 LLVTELLAVTNVLLMNLIIAMFSYTFVQVQGNADMFVKFQRYNLIYVHERPALAPPFILL 1015
Qy 1018 SHLSLTLRRVFKKEAEHREHLERDLDPDLDQKVVTWETVOKENFLSKMKRRRDSGEV 1077
Db 1016 SHLSLVLKQVFRKEAQHRLERDLDPDLDQKIITWETVOKENFLSKMKRRRDSGEV 1075
Qy 1078 LRKTAHRVDIAKYLGLREQEKRIKLESQINVCVSVLSSVADVLQAGGSPSSOHCGE 1137
Db 1076 LRKTAHRVDIAKYLGLREQEKRIKLESQINVCVSVLSSVADVLQAGGSPSSOHCGE 1135
Qy 1138 GSQVLAADHRGGLDGEQPGAGQPPSDT 1165
Db 1136 RSQPASADREYLE-----SGLPPSDT 1157
RESULT 13
ADR87165
ID ADR87165 standard; protein; 1156 AA.
XX ADR87165;
AC ADR87165;
DT 02-DEC-2004 (first entry)
XX Rat betaTRP amino acid sequence, seq id 6.
DE Antidiabetic; betaTRP modulator; gene therapy; glucose; insulin; betaTRP;
XX beta transducin; diabetes; type 2; rat.
KW Rattus sp.
XX WO2004079372-A1.
XX 16-SEP-2004.
XX 04-MAR-2004; 2004WO-US006697.
XX 05-MAR-2003; 2003US-0452596P.
XX (META-) METABOLEX INC.
XX Johnson JD, Zhou Y;
XX WPI; 2004-668668/65.
XX N-PSDB; ADR87164.
XX Identifying agents that induce glucose-stimulated insulin production in
an animal, useful for treating diabetes, comprises contacting an agent to
a polypeptide and selecting an agent that binds or enhances its
expression/activity.
XX Disclosure; SEQ ID NO 6; 83pp; English.
XX The invention relates to a method for identifying an agent that induces
glucose-stimulated insulin production in an animal. The method comprises
contacting an agent to a betaTRP polypeptide, and selecting an agent that
binds to it or enhances its expression or activity. Further disclosed is
a method for expressing betaTRP (beta-transducin protein) in a pancreatic
islet cell. The method is useful for identifying an agent that induces
glucose-stimulated insulin production in an animal, and thus treating
individuals having type 2 diabetes mellitus or having a predisposition
for it. The current sequence represents the rat betaTRP amino acid
sequence.
XX Sequence 1156 AA;
Query Match 82.5%; Score 5025.5; DB 8; Length 1156;
Best Local Similarity 83.0%; Pred. No. 0;
Matches 968; Conservative 75; Mismatches 112; Indels 11; Gaps 3;

Qy	1	MODVQPPGPGDAEDRRELCLHRGEVNFQSGKKRGKFPVRVPSGVAPSVLPDLLLAEB	60
Db	1	MPMAQSSCPGSPDPDTCGDGWEVPVLCCKGEVNFQSGKKRGKFPVKVPSNVAPSMLEPILLTJEW	60
Qy	61	HLPAPNLVVSVLGBEQPFAMKSWLDVLKGLVKAAQSTGAWILTSALRVGLARHVGOAV	120
Db	61	HLPAPNLVVSVLGBEERLFAMKSWLDVLKGLVKAAQSTGAWILTSALRVGLARHVGOAV	120
Qy	121	RDHSLASTSTKRVVAVQMASLGRVLHRRILIEEAQEDFPVHYPPDDGSGQGPLCSLDSNL	180
Db	121	RDHSLASTSTKRVVAVIOWMASLDRILHRLQLLDGVQEDTPIHYPADEGSTQGFPLCPFLDSNL	180
Qy	181	SHFLTIVBPGPKG-DGLTELRLRLKHI SEORAGYGGTSGIEIETPVLCILVNGDPNTLER	239
Db	181	SHFLTIVBPGTUGSNGDGLAEIQLSLERHISQORTGYGTSIQIETPVLCILVNGDPSTLER	240
Qy	240	ISRAVEQAAPWLLILVSGGCIADVLAAALVNQPHLVPKVAEKQFKPKPSKHFSMEDIVRW	299
Db	241	MSRAVEQAAPWLLLAGSGGIADVLAAALVQGPHELLVPVTEKQPREKPFSECFSEWAIVHW	300
Qy	300	TKLQNTTSHOHLTVYDFPQEGGSEELDTVILKALVKACKSHSGEPQDYLDELKLAAMD	359
Db	301	TELLQNTAAHPHLLTVYDFEQGSEEDLTVILKALVKACKSHSRDAQDYLDELKLAAMD	360
Qy	360	RVDIAKSIENGDIWEMKSCDLEEVWVDALVSNKEPEFVRLFVDNGADVADFTYGRLOELY	419
Db	361	RVDIAKSIENGDIWEMKSCDLEEVWMTDALVSNKPDVRLFVDSGADWAEFTYGRLOELY	420
Qy	420	RSVSRKSLFOLLQKQBEARLTLAGLGTQARPPAPPAFSLHEVSRVLKDFLQDADR	479
Db	421	HSVSPKSLFELLERKGEERLTLAGLGAQQTRELPGLPAPSLHEVSRVLKDFLHADR	480
Qy	480	GFYQDGRDRRRAEKGPAPKPTQKMLLDLNQKSENPMWRDLFLWAVLQNRHEMATYFWA	539
Db	481	GFYQDG----RMEERGPPEKGPAGQKMLPDLRSKSEDPWRDLFLWAVLQNRHEMATYFWA	536
Qy	540	MGQSGVAAALAAKILKEMSHLEYEAFAARATREAKYERLALDIFSECYNSEARAFALL	599
Db	537	MGRSGVAAALAAAKIIKEMSHLEKBAEVARTMRBAKEYEQALDIFSECYNSEARAFALL	596
Qy	600	VRNRNCSKTTCLHLATEADAKAFADHGVOQAFTRIWWGDMMAAGTPTLRLILGALFPCAL	659
Db	597	VRNRHNSRTTCLHLATEADAKAFADHGVOQAFTKIWWGDMATGTPTLRLILGALFPCAL	656
Qy	660	VYTNLIITFSEBAPRTGLEDLQDLSLDTESKPIYGLQSRVEELVEAPRAQGDGRPAVF	719
Db	657	IYTNLIISFSEDAPQRMLEDLQEPDSDLMESKSFICSHGGQLEKLTZAPRAPGDLGPQAAF	716
Qy	720	LLTRWRKFWGAPVTVELGNVVMYFAFLFTYVLLVDPRPQGPSPGPEVTLYFWVFTLV	779
Db	717	LLTRWRKFWGAPVTVELGNVVMYFAFLFTSVLLVDPRPQGPSPGSEVTLYFWVFTLV	776
Qy	780	LEETROGFFTDETHLVKKFTLYVGDNNWKNCDMAIFLFVGVTCRMLPSAFEAGRTVLA	839
Db	777	LEETROGFFTNEDTRLVKFTLYVYEDNNWKNCDMAIFLFVGVTCRVMVPSVFEAGRTVLA	836
Qy	840	MDFMVFTLRLIHPAIHQKGPKIIIVVERMMKOVFFLFFLSVWLVAYGVTQTALLPHD	899
Db	837	IDFMVFTLRLIHPAIHQKGPKIIIVVERMMKOVFFLFFLSVWLVAYGVTQTALLPHD	896
Qy	900	GRLEWIFRRVLYRPLYQIFQOIPUDEIDEARVNCSTHPLLEDSPSCPSLYANWLVLLL	959
Db	897	GRLEWIFRRVLYRPLYQIFQOIPUDEIDEARVNCSTHPLLEDSSCPNLYANWLVLLL	956
Qy	960	VTFLLVNTVLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIIVEYHRRPALAPPFILLSH	1019
Db	957	VTFLLVNTVLLMNLIIAMFSYTFQVQVQGNADMFWKFORYHLIIVEYHGRPALAPPFILLSH	1016
Qy	1020	LSLTILRVFPKKEABKHEHLERDLPDLDQKVTVTWEVQKENFLSKMKERRRDSGEVLR	1079
Db	1017	LSLVLKQVFRKEAQHKQHLERDLPDVPDQKIIITWETVQKENFLSTWKEKRRRDSGEVLR	1076

QY	1080	KTARVDFPIAKYLGGLREQEKRIKCLSEQINYSVLSSVADVLAQGGPRRSHQCGEGS	1133
Db	1077	KTARVDFLIIAKYIIGGLREQEKRIKCLSEQANYCMLLLSSMTDTLAPGTYSSQNCGRSS	1136
QY	1140	QLVAADHRGGLDGWEQPGAGOPPSDT	1165
Db	1137	QPASARDREYLE-----AGLPHSDT	1156
RESULT 14			
ID	ABB83853		
ID	ABB83853	standard; protein; 1164 AA.	
AC	ABB83853;		
DT	30-SEP-2002	(first entry)	
XX			
DE	Rat L-TRP	SEQ ID NO 2.	
XX			
KW	Rat; L-TRP;	taste; cell signalling; TC-ICS; food; pharmaceutical;	
KW	taste	cell-specific ion channel subunit.	
XX			
OS	Rattus sp.		
XX			
OS	W0200254069-A1.		
PN			
PD	11-JUL-2002.		
XX			
PF	26-DEC-2001;	2001WO-US049808.	
XX			
PR	29-DEC-2000;	2000US-0259379P.	
PR	21-DEC-2001;	2001US-00026188.	
XX			
PA	(SEGC)	UNIV CALIFORNIA.	
XX			
PI	Zuker CS,	Zhang Y;	
XX			
DR	WPI;	2002-583632/62.	
DR	N-PSDB;	ABN85732.	
XX			
PT	Identifying	modulators of taste signaling in taste cells for use in food	
PT	and	pharmaceutical industries to customize and regulate taste, by	
PT	determining	effect of the compound on a taste cell-specific ion channel	
PT	subunit.		
XX			
PS	Claim 1;	Page 63; 306pp; English.	
XX			
CC	The	invention relates to identifying (M1) a compound that modulates taste	
CC	signalling	in taste cells, by contacting the compound with a eukaryotic	
CC	host	cell or cell membrane which expresses a taste cell-specific ion	
CC	channel	subunit (TC-ICS), and determining a functional effect of the	
CC	compound	upon a transmembrane ion flux of a predetermined ion,	
CC	identifying	a compound that modulates taste signaling in taste cells.	
CC	(M1)	is useful for identifying a compound that modulates taste signalling	
CC	in	taste cells, for identifying a compound that binds to a taste cell	
CC	specific	ion channel subunit and for modulating taste signaling in taste	
CC	cells	of a mammal, in particular a human. Modulators identified by (M1)	
CC	are	used by the food and pharmaceutical industries to customize taste,	
CC	e.g.	as additives to food or medicine so that the food or medicine tastes	
CC	different	to the subject who ingests it. Bitter medicines can be made to	
CC	taste	less bitter and sweet substance can be enhanced. The modulators are	
CC	useful	for pharmacological and genetic modulation of taste signalling	
CC	pathways.	The taste modulators can be directly administered to mammalian	
CC	subjects	for modulation of taste in vivo. The present sequence is that of	
CC	the	rat L-TRP protein of the invention	

Db 9 MPMAQSSCFSPDPTGDGWEFVLCGEVNFVSGSKRSKFVKVSNVAPSMLELLTTEW 68
Qy 61 HLPAPNLVSVLGEQPPFAMKSWLRDLVRKGLVKAQSTGAWILTSALRGLARHVQAV 120
Db 69 HLPAPNLVSVLGEERLFAKMSWLRDLVRKGLVKAQSTGAWILTSALHGLARHVQAV 128
Qy 121 RDHSLASTSTKRVVAVGMSIGRVLHRRILIEEAQEDPPVHPEDDGGSGPLCLSDSNL 180
Db 129 RDHSLASTSTKRVVAVGMSIGRVLHRRILIEEAQEDPPVHPEDDGGSGPLCLSDSNL 188
Qy 181 SHFILVEGPPGKG-DGILTELRLRLKHISEORAGYGGTGSIEIPVLCCLVNGDPNTLER 239
Db 189 SHFILVEGTTGSGNDGLAEQLSLEKHSQRTGYGGTSSIQIPVLCCLVNGDPSTLER 248
Qy 240 ISRAVEQAAPMLILVSGGIDVLAALVNQPHLLVPKVAEQFKKFPKSFHSEDIWRV 299
Db 249 MSRAVEQAAPMLILAGSGGIADVLAALVQPHLLVPQVTEKQFKEKFPSECFSEWAI VHW 308
Qy 300 TKLLONITSHOHLITVDFEQQSGSELDVTILKALVKACKSHSQPQDYLDLKLAVAMD 359
Db 309 TELLQNTAAHPHLLITVDFEQQSGSELDVTILKALVKACKSHSRDAQDYLDLKLAVAMD 368
Qy 360 RVDIAKSEIFNGDVWKSCDLEEVNMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELY 419
Db 369 RVDIAKSEIFNGDVWKSCDLEEVNMDALVSNKPEFVRLFDVNGADMAEFITYGRLOELY 428
Qy 420 RSVRSKSLFOLLQKQBEARLTLAGLGTQQAAREPPAGPPAPSLHEVSRVLKDFLODACR 479
Db 429 HVSVPKSLFELLERKHEEGRLLTAGLGAQQRKLPVGLPAPSLHEVSRVLKDFLHDACR 488
Qy 480 GRYQGRPGDRRAEKPAKRTGQKWLIDLNKSENPRDLFWAVLQNRHEMATYFWA 539
Db 489 GRYQDG----RMEKRGPKRPAGQKWLIDLNKSENPRDLFWAVLQNRHEMATYFWA 544
Qy 540 MGOEGVAAALACKILKEMSHLETAEAAARATREAKYERLALDLFSECVSNSEARAFALL 599
Db 545 MREGVAAALACKILKEMSHLEKEAEVARTWREAKYEQALDLFSECVSNSEARAFALL 604
Qy 600 VRRNRCSKTTCLHLATEADAKAFPAHGVQVAPLRIWGMGMAAGTPILRLGAFCLPAL 659
Db 605 VRRNHSWRTTCLHLATEADAKAFPAHGVQVAPLRIWGMGMAAGTPILRLGAFCTPAL 664
Qy 660 VTNLITPSEAPLRTGLDQLDLSLDEKSPGLQSRVELVEAPRAQDRGPRAVF 719
Db 665 IYTNLISFSEDAPQRMDELQEPDSDLMKESFLCSHGQLEKLEAPRAPGDLGPQAAF 724
Qy 720 LLTRWRKFGAPVTVFLGNVVMYFAFLFTVTVLLVDFRPPQPGSGPBTLYLFWVFTLV 779
Db 725 LLTRWRKFGAPVTVFLGNVVMYFAFLFTVTVLLVDFRPPQPGSGSEVTLVFWVFTLV 784
Qy 780 LBEIRQGFTEDETHLVKFTLYLVGNMKNCDMAIFLFIIVGTCRMLPSAFEAGRTVLA 839
Db 785 LBEIRQGFTEDETHLVKFTLYLVGNMKNCDMAIFLFIIVGTCRMLPSAFEAGRTVLA 844
Qy 840 MFMVFTLRIHIFAIHKGOLGPKIIVERRMKDVPFFLFLSVLWVAYGVTQALLHPHD 899
Db 845 IDPMVFTLRIHIFAIHKGOLGPKIIVERRMKDVPFFLFLSVLWVAYGVTQALLHPHD 904
Qy 900 GRLEWIFRVLRYPLQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVLILL 959
Db 905 GRLEWIFRVLRYPLQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVLILL 964
Qy 960 VTELLVTNLLMNLIIAMFSYTFQVQGNADMFKEQRYNLIIVEYHERPALAPFFILLSH 1019
Db 965 VTELLVTNLLMNLIIAMFSYTFQVQGNADMFKEQRYNLIIVEYHERPALAPFFILLSH 1024
Qy 1020 LSLTLARVFKKEAEHKEHLERLDPLDPLQKVTWETVQENFLSKWEKRRRSESEVLR 1079
Db 1025 LSLVLQVFRKEAQHQLERLDPDQKIIITWETVQENFLSKWEKRRRSESEVLR 1084
Qy 1080 KTAHRVDPIAKYGLGLEQEKRIKCLSEQINYSVLSSVADVLAQGGGPRSSQHCGES 1139

Db 1085 KTAHRVDLIAKYTGLLEQEKRIKCLSEQINYSVLSSVADTILAPGTYSSSQNCGRS 1144
Qy 1140 QLVAADHRGCLDGWEQPGAGQPPSDT 1165
Db 1145 QPASARDREYLE-----AGLPHSDT 1164
RESULT 15
AAB86163
ID AAB86163 standard; protein; 872 AA.
XX
AC AAB86163;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human MTR1 protein without exon 18 fragment.
XX
KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
KW lip15.5 abnormality; chromosome 11; anticancer; developmental activity;
KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;
KW cell growth; cell death; cell differentiation; urogenital disease;
KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
KW rhabdomyosarcoma.
XX
OS Homo sapiens.
XX
FN WO200132693-A2.
XX
PD 10-MAY-2001.
XX
PF 06-NOV-2000; 2000WO-DE003876.
XX
PR 04-NOV-1999; 99DE-01053167.
XX
PA (UYGU-) UNIV GUTENBERG JOHANNES.
XX
PI Prawitt D, Pelletier J, Zabel B;
XX
DR WPI; 2001-316417/33.
XX
DR N-PSDB; AAH20574.
XX
PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
XX syndrome and tumors, also related proteins and antibodies.
XX
PS Claim 10; Fig 4; 46pp; German.
XX
CC This invention describes a novel DNA sequence (I) encoding the MTR1
CC protein that: (i) has at least one biological activity of a TRP
CC (transient receptor potential) family protein; (ii) is connected with
CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC with tumors involving lip15.5 abnormalities. The products of the
CC invention have anticancer and developmental activity. MTR1 is involved in
CC regulation of intracellular calcium ion levels, which are essential for
CC cellular responses to hormones and/or growth factors; also in apoptosis
CC and cell growth, death and differentiation, and in urogenital diseases,
CC including polycystic kidney disease. (I) and related ribozymes, antisense
CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
CC associated with altered expression of the MTR1 gene or activity of its
CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
CC used for diagnosis of such diseases. (I) can also be used for recombinant
CC production of MTR1 proteins (II) (used for analysis, characterization and
CC therapy), as tissue or chromosomal markers, for identifying genetic
CC diseases and related sequences, as primers for genetic fingerprinting, as
CC source of oligonucleotides for biochips, and to raise anti-protein or
CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
CC competitive assays for (II), as tissue markers; for identifying
CC interacting proteins and in screening for (ant)agonists. This sequence
CC represents a human MTR1 protein described in the method of the invention
XX
SQ Sequence 872 AA;

Query Match		74.4%	Score 4534;	DB 4;	Length 872;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 869;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MDVQGP	RRPGSGDAEDRRRLGLHGRGEVNF	GGGKRGKRV	PSGVAPSVLFDLLLAEW 60
Qy	61	HLFAPNLV	SLVGEQPFAMKSWLRDVLKGLVKA	AQSTGAMITLSALRVGLARHVQAV 120	
Db	61	HLFAPNLV	SLVGEQPFAMKSWLRDVLKGLVKA	AQSTGAMITLSALRVGLARHVQAV 120	
Qy	121	RDHSLAST	TKVRVAVGASLGRVLRHRIIEA	QEDFPVHYPEDDGGSGGPLCSLDSNL 180	
Db	121	RDHSLAST	TKVRVAVGASLGRVLRHRIIEA	QEDFPVHYPEDDGGSGGPLCSLDSNL 180	
Qy	181	SHFILVEP	PGPGKGDGLTELRLRLEKHISE	QAGYGGTGSIBIPVLC	LVNGDPNTLRI 240
Db	181	SHFILVEP	PGPGKGDGLTELRLRLEKHISE	QAGYGGTGSIBIPVLC	LVNGDPNTLRI 240
Qy	241	SRAVEQA	APWLLILVSGGGIADVLAAVN	PHLLVPKVAEKQKEKPPSKHFSWEDIVRWT 300	
Db	241	SRAVEQA	APWLLILVSGGGIADVLAAVN	PHLLVPKVAEKQKEKPPSKHFSWEDIVRWT 300	
Qy	301	KLLQNT	TSQHLLTVYDFQEGSEELDTVIL	KALKACKSHSQEQDYLDLKLAVADR 360	
Db	301	KLLQNT	TSQHLLTVYDFQEGSEELDTVIL	KALKACKSHSQEQDYLDLKLAVADR 360	
Qy	361	VDIAKSEI	ENGDEVKSCDLEEMVDALVSN	KPEFVRLFVNGADVADFLTYGRLOELYR 420	
Db	361	VDIAKSEI	ENGDEVKSCDLEEMVDALVSN	KPEFVRLFVNGADVADFLTYGRLOELYR 420	
Qy	421	SVSRKSL	LDLQKQEEARLTLAGLTCQ	AREPPAGPPAFSLHEVSRVLKDFLODACRG 480	
Db	421	SVSRKSL	LDLQKQEEARLTLAGLTCQ	AREPPAGPPAFSLHEVSRVLKDFLODACRG 480	
Qy	481	FYQDGP	GGRRRAEKGPAKPTGQKWL	LDLNQKSENPRDLFLMAVLQNRHEMATYFWAM 540	
Db	481	FYQDGP	GGRRRAEKGPAKPTGQKWL	LDLNQKSENPRDLFLMAVLQNRHEMATYFWAM 540	
Qy	541	GQGVAA	LAACKILKEMSHLETEA	AAATREAKYERLALDLFSECYSNSEARAFALLY 600	
Db	541	GQGVAA	LAACKILKEMSHLETEA	AAATREAKYERLALDLFSECYSNSEARAFALLY 600	
Qy	601	RNRCSKT	TCIHLATEADAKAF	AHDGVQAFTRIWMGMAAGTPIILRLGAFLCPALV 660	
Db	601	RNRCSKT	TCIHLATEADAKAF	AHDGVQAFTRIWMGMAAGTPIILRLGAFLCPALV 660	
Qy	661	YTNLIT	FSSEAPLRTGLEDLQDLS	LDTSEKSPLYGLQSRVEELVEAPRAQDGRPAVFL 720	
Db	661	YTNLIT	FSSEAPLRTGLEDLQDLS	LDTSEKSPLYGLQSRVEELVEAPRAQDGRPAVFL 720	
Qy	721	LTRMRK	FWGAPVTVPLGNVMYFAFL	FTYVLLVDFRPPPGSGPEVTLYFWVFTVLV 780	
Db	721	LTRMRK	FWGAPVTVPLGNVMYFAFL	FTYVLLVDFRPPPGSGPEVTLYFWVFTVLV 780	
Qy	781	BEIRQGF	TDETHLVKKFTLYVGN	NKCDMVAIFLFI	VGVTCTMLPSAFEAGRTVLAM 840
Db	781	BEIRQGF	TDETHLVKKFTLYVGN	NKCDMVAIFLFI	VGVTCTMLPSAFEAGRTVLAM 840
Qy	841	DFMVFT	LRLIHIFAIHKQLGPKI	IVVERM 869	
Db	841	DFMVFT	LRLIHIFAIHKQLGPKI	IVVERM 869	

Search completed: June 22, 2005, 18:15:39
Job time : 184 secs

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OM protein - protein search, using sw model

Run on: June 22, 2005, 18:09:49 ; Search time 45 Seconds
(without alignments)
1932.581 Million cell updates/sec

Title: US-09-834-792D-4
Perfect score: 6093
Sequence: 1 MQDVQPRPGSGDAEDRE.....HRGGLDGEQPGAGPPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	6093	100.0	1165	4	US-09-949-016-6874
2	6085	99.9	1165	4	US-09-949-016-11392
3	2040	33.5	1529	4	US-09-949-016-11100
4	2039	33.5	1503	4	US-09-600-087-2
5	2039	33.5	1503	4	US-09-949-016-6341
6	1566.5	25.7	1095	3	US-09-112-096-15
7	1566.5	25.7	1095	4	US-09-636-215-778
8	1566.5	25.7	1095	4	US-09-685-166A-778
9	1566.5	25.7	1095	4	US-09-679-426-778
10	1566.5	25.7	1095	4	US-09-759-143-778
11	1566.5	25.7	1095	4	US-09-651-236-778
12	1558.5	25.6	1095	4	US-09-636-215-780
13	1558.5	25.6	1095	4	US-09-685-166A-780
14	1558.5	25.6	1095	4	US-09-679-426-780
15	1558.5	25.6	1095	4	US-09-759-143-780
16	1558.5	25.6	1095	4	US-09-651-236-780
17	1240.5	20.4	1533	1	US-08-623-679-9
18	1240.5	20.4	1533	3	US-08-933-774-9
19	1240.5	20.4	1533	3	US-09-181-030-9
20	1240.5	20.4	1533	3	US-09-534-242-9
21	1240.5	20.4	1533	3	US-09-454-854-9
22	1240.5	20.4	1533	3	US-09-164-671-9
23	1240.5	20.4	1533	4	US-09-182-113-9
24	1240.5	20.4	1533	4	US-08-862-442-9
25	1162.5	19.1	1497	1	US-08-623-679-7
26	1162.5	19.1	1497	3	US-08-933-774-7
27	1162.5	19.1	1497	3	US-09-181-030-7

28	1162.5	19.1	1497	3	US-09-534-242-7	Sequence 7, Appli
29	1162.5	19.1	1497	3	US-09-454-854-7	Sequence 7, Appli
30	1162.5	19.1	1497	3	US-09-164-671-7	Sequence 7, Appli
31	1162.5	19.1	1497	4	US-09-182-113-7	Sequence 7, Appli
32	1162.5	19.1	1497	4	US-08-862-442-7	Sequence 7, Appli
33	820	13.5	315	3	US-09-020-956-112	Sequence 112, App
34	820	13.5	315	3	US-09-030-607-112	Sequence 112, App
35	820	13.5	315	3	US-09-439-313-112	Sequence 112, App
36	820	13.5	315	3	US-09-352-616A-112	Sequence 112, App
37	820	13.5	315	4	US-09-232-149A-112	Sequence 112, App
38	820	13.5	315	4	US-09-159-812-112	Sequence 112, App
39	820	13.5	315	4	US-09-636-215-112	Sequence 112, App
40	820	13.5	315	4	US-09-685-166A-112	Sequence 112, App
41	820	13.5	315	4	US-09-115-453-112	Sequence 112, App
42	820	13.5	315	4	US-09-688-489-112	Sequence 112, App
43	820	13.5	315	4	US-09-679-426-112	Sequence 112, App
44	820	13.5	315	4	US-09-759-143-112	Sequence 112, App
45	820	13.5	315	4	US-09-651-236-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-09-949-016-6874
; Sequence 6874, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6874
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6874

Query Match	100.0%;	Score 6093;	DB 4;	Length 1165;		
Best Local Similarity	100.0%;	Pred. No.: 0;				
Matches 1165;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1	MODVQPRPGSGDAEDRE	RLGLHGEVNF	FGSGKKRGKFKFVRVPSGVA	SVLFDLLAEW 60	
Db	1	MODVQPRPGSGDAEDRE	RLGLHGEVNF	FGSGKKRGKFKFVRVPSGVA	SVLFDLLAEW 60	
Qy	61	HLPAPELVSLVGEEROP	FAMKSWLRDLVRKGLVKAQA	SGMTLTSALRGLARHVGQAV	120	
Db	61	HLPAPELVSLVGEEROP	FAMKSWLRDLVRKGLVKAQA	SGMTLTSALRGLARHVGQAV	120	
Qy	121	RHSLASTSTKRVVAVG	WASLGRVLRHRI	LEEAQEDFFVHPEDDGGSG	QGPLCSLDSNL 180	
Db	121	RHSLASTSTKRVVAVG	WASLGRVLRHRI	LEEAQEDFFVHPEDDGGSG	QGPLCSLDSNL 180	
Qy	181	SHFILVEPPGPKGDL	TELRLEKHI	SEORAGYGGTGSIEIPVLC	LLVNGDPNTERI 240	
Db	181	SHFILVEPPGPKGDL	TELRLEKHI	SEORAGYGGTGSIEIPVLC	LLVNGDPNTERI 240	
Qy	241	SRAVEQAAPWLLV	GGGIADVLAALVN	QPHLLVPKVAEKQKFKPS	KHFSWEDIVRWT 300	
Db	241	SRAVEQAAPWLLV	GGGIADVLAALVN	QPHLLVPKVAEKQKFKPS	KHFSWEDIVRWT 300	
Qy	301	KLQNITSHOHLTV	YDFEGSGEELDT	VILKALVKACKSHSQBP	QDYLDELKLA	VAWDR 360

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301 KLLQNTTSHQHLTVYDFEQSGSELDVTILKALVKACKSHSQEPDQVLDLKLAVADR 360
361 VDIKSEIFNGDVEWKSCLSEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYR 420
361 VDIKSEIFNGDVEWKSCLSEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYR 420
421 SVSRKSLLLFDLQKQEBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
421 SVSRKSLLLFDLQKQEBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
481 FYQDGRPGDRRAEKGPAKRTGQKWLDDLNQKSENPMWDLFLMAVLQNRHEMATYFWAM 540
481 FYQDGRPGDRRAEKGPAKRTGQKWLDDLNQKSENPMWDLFLMAVLQNRHEMATYFWAM 540
541 QGEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLV 600
541 QGEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLV 600
601 RNRCSKTTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPILRLLAGAFLCPALV 660
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661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRGPRAVFL 720
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721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYTVLLVDFRPPQSGSGPEVTLYFWVFTLV 780
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841 DFMVFTLRLIHFIAHKQLGPKIIVVERMMKDVFFLFFLSVNLVAVGVTQTQALLHPHDG 900
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1021 SLTLRRVFKBAEAKHREHLERDLPDLQKVVTVTQENFNLKWKERRRDSSEVLRLK 1080
1081 TAHRVDFPIAKYLGRLREGEKIKLESQINYCSVLVSSVADVLAQGGQPSRSHQCGSQ 1140
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1141 LVAADHRGGLDGEQPGAGQPPSDT 1165

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RESULT 2
US-09-949-016-11392
; Sequence 11392, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11392
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11392

Query Match          99.9%; Score 6085; DB 4; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 181 SHFILVEPGPGKGDGLTELRLLEKHSIORAGYGGTSGIEIPVLCCLVNGDPNTLERI 240
Db 181 SHFILVEPGPGKGDGLTELRLLEKHSIORAGYGGTSGIEIPVLCCLVNGDPNTLERI 240
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Qy 301 KLLQNTTSHQHLTVYDFEQSGSELDVTILKALVKACKSHSQEPDQVLDLKLAVADR 360
Db 301 KLLQNTTSHQHLTVYDFEQSGSELDVTILKALVKACKSHSQEPDQVLDLKLAVADR 360
Qy 361 VDIKSEIFNGDVEWKSCLSEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYR 420
Db 361 VDIKSEIFNGDVEWKSCLSEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYR 420
Qy 421 SVSRKSLLLFDLQKQEBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
Db 421 SVSRKSLLLFDLQKQEBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
Qy 481 FYQDGRPGDRRAEKGPAKRTGQKWLDDLNQKSENPMWDLFLMAVLQNRHEMATYFWAM 540
Db 481 FYQDGRPGDRRAEKGPAKRTGQKWLDDLNQKSENPMWDLFLMAVLQNRHEMATYFWAM 540
Qy 541 QGEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLV 600
Db 541 QGEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLV 600
Qy 601 RNRCSKTTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPILRLLAGAFLCPALV 660
Db 601 RNRCSKTTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPILRLLAGAFLCPALV 660
Qy 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRGPRAVFL 720
Db 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRGPRAVFL 720
Qy 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYTVLLVDFRPPQSGSGPEVTLYFWVFTLV 780
Db 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYTVLLVDFRPPQSGSGPEVTLYFWVFTLV 780
Qy 781 BEIRQGFPTDEDTHLVKKFTLYVGDNNKCDMAIFLFIIVGTCRMLPSPAFAEAGRTVLAM 840
Db 781 BEIRQGFPTDEDTHLVKKFTLYVGDNNKCDMAIFLFIIVGTCRMLPSPAFAEAGRTVLAM 840
Qy 841 DFMVFTLRLIHFIAHKQLGPKIIVVERMMKDVFFLFFLSVNLVAVGVTQTQALLHPHDG 900

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Db 841 DFMVFTLLRIHFAHKQGLGKFIIVVERMKDVFVFLSVMLVAVGVTTOALLPHDG 900
Qy 901 RLEWIFRVLRYPIQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLY 960
Db 901 RLEWIFRVLRYPIQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLY 960
Qy 961 TFLVTVNVLNLLIAMESTYFQVQGNADMFVFORNLIVEHERPALAPPTILLSHL 1020
Db 961 TFLVTVNVLNLLIAMESTYFQVQGNADMFVFORNLIVEHERPALAPPTILLSHL 1020
Qy 1021 SLTLRRVFKAEHREHLERDLPDLPDQKVVTWETVQENFLSKWEXRRDSEGEVLK 1080
Db 1021 SLTLRRVFKAEHREHLERDLPDLPDQKVVTWETVQENFLSKWEXRRDSEGEVLK 1080
Qy 1081 TAHRVDFIAKYLGLRQEKRIKLESQINVCVSVLVADVLAQGGGPRSSQHCGEQ 1140
Db 1081 TAHRVDFIAKYLGLRQEKRIKLESQINVCVSVLVADVLAQGGGPRSSQHCGEQ 1140
Qy 1141 LVADHRGGLDGEQPGAGQPPSDT 1165
Db 1141 LVADHRGGLDGEQPGAGQPPSDT 1165

RESULT 3

US-09-949-016-11100
; Sequence 11100, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11100
; LENGTH: 1529
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11100

Query Match 33.5%; Score 2040; DB 4; Length 1529;
Best Local Similarity 38.8%; Pred. No. 1,7e-190;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;
Qy 26 GEVFGSGKGRKFKVRVPSGVAPSVLFDLLAEHLPAPNLVSLVGBEEQPFAMKSWLR 85
Db 154 GDIVFTGLGQVKVYRVSDPTSSVYHLMTHQWGLDVPNLLISVYTGAKFNKMPREK 213
Qy 86 DVLKGLVKAQSTGAWILTSALRVGLARHVGQAVRDHSLASTSTKRVVAVGMSLGRV 145
Db 214 SIFRGLVKVQTTGAWIITGSGHTGVKMQVGEARDFSLSSYKEGELITIGVATWGTV 273
Qy 146 LHRRIIEAQEDPVMVHPEDDGGSQGPLCLSDNSHLNFILVEPGPKGDGLTEHLRL 205
Db 274 HRREGLIHPGSPFAEYILDEG-QGNLTCLDSNHSFHLVDDGTHGQGVETPLRL 332
Qy 206 KHTSEQAGVGGTSTETPVLCLLVGDPNLTLEISRVAEQAPWLLVSGSGIADVLAA 265
Db 333 KFISEQTKERGGV-AIKIPVVCVLEGGPGTLTINATNGTPCVVVGSGRVDVIAQ 391
Qy 266 LVNQP--HLVVPKVAEQ---FKEKFPKSHFSEWEDIVRMTKLLQNITSHOHLTVYDFEQ 320
Db 392 VANLPVSDITISLIQOKLSVFFQEMFET--FTESRIVEWTKIQDIVRRRQLLTVFREK 449

Qy 321 EGSEELDTVLKALVACKSHSQEPDYLD-ELKLVANDRVDIKASEIFNGDVEWKSCD 379
Db 450 DQQQDVDAJLQALLKASRQDHPGHQWDLQKLVAMNRVDIARSEIFMDEWQKPSD 509
Qy 380 LEEVWDALVSNKDFEVRFLFDGADVADFTYGRLOELYSRKSILLPDLLOKQBEA 439
Db 510 LHPTMTAALISNKEFEVKLFLENGVQLKEFVTWDTLLYENLDPSCFLSHKLOK----- 564
Qy 440 RLTLAGLGTQARPPAGP--PAPSLHEVSRLKDFLQDACRGFYQDGRPDRRR----- 492
Db 565 -----VLVEDPERPACAPAPRLQMHVAVQLRELLGDFTPPLYPRPHNDRLLLPV 618
Qy 493 -----AEKGPARKPTGCKWLLDLNQKSENPWDLFLWAVLQNHENATYFWAMQ 542
Db 619 PHVKLVQGVSLRSLYKRSGHVTF-----TMDPIRDLTLIWAIVQNRRELAGIWAQSQ 672
Qy 543 EGVAALAAACKIKEMSHLETEAAR---ATREAKYERLALDLFSECSNSEARAFALL 599
Db 673 DCIAAALACSKIKELSKKEEDTDSSEMLALAE-EYEHRAIGVFTECYRDEERAQKLL 731
Qy 600 VRNRCSKTTCLHLATEADAKAFFAHDGVQAFTRIWMGDMAAGTPIRLGLGAPLCPAL 659
Db 732 TRVSEANGKTTCLQALEAKDMKFVSHGIGQAFLLKVMWGLSVNDGLWRVTLCLAPPL 791
Qy 660 VYTNLITFSEEARLRTGLELDLSDLTEKSPLYGLQSRVEELVEAPRAQDGRPRAVF 719
Db 792 LLTGLISPREKR-----LQD-----VGTFAA----- 812
Qy 720 LLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPPQSGSGEVTLTYFWFTLV 779
Db 813 ---RARAFPTAPVVVFLNLSYFAFLCFAYVLMVDFQV---PSWCEAIYLMFLSLV 866
Qy 780 LEEIRQGFPTDDBTHLVKKFTLYGDNMKNCDWAIFFIVGVTCTRMFLPSFAEAGRTVLA 839
Db 867 CEMRQLFYDDECCLMKKAALYFDFWNLVDGAILLFVAGLTCRLIPATLYPGRVILLS 926
Qy 840 MDMVFTLRLIHFAHKQGLGKFIIVVERMKDVFVFLSVMLVAVGVTTOALLPHD 899
Db 927 LDFILFCLRLMHIFTISKTLGPKIIVKRMKMDVFVFLFLAVVYVSEGAQAQILHNE 986
Qy 900 GRLEWIFRVLRYPIQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLY 948
Db 987 RRVDFRGLVAVVSHYLTIFGQIPGIDGVNFPNHCSPNGTDPY-----KPKCESDATQ 1042
Qy 949 ---LYANVLVILLVTFLLVTVNVLNLLIAMESTYFQVQGNADMFVFORNLIVEHER 1006
Db 1043 RPAFPPELTVLLCLYLLFTNILLNLLIAMESTYFQVQGNADMFVFORNLIVEHER 1102
Qy 1007 RPAAPPFILLSLTLRRVFKAEHREHLERDLPDLPDQKVVTWETVQENFLSKW 1066
Db 1103 RPAAPPFILLSLTLRRVFKAEHREHLERDLPDLPDQKVVTWETVQENFLSKW 1162
Qy 1067 EKRRDSEGEVLRKTAHRVDFIAKYL-----GGLREQEKRIKLESQINVCVSVLVSS 1118
Db 1163 QPQOKRQEPKEDISNVDAMVMDLLDPLKRSQSM-----EQLASLEEQVQAQALHW 1219
Qy 1119 VADVLAQGGGPRSSQHCGEQSVLVAAD---HRGGLDGEWQPG 1157
Db 1220 IVRTLRSAGSSEADVPTLASQAAAEEDPAEFGGRKTEEPG 1261

RESULT 4

US-09-600-087-2
; Sequence 2, Application US/09600087
; Patent No. 6548272
; GENERAL INFORMATION:
; APPLICANT: Shimizu, No. 6548272uyoshi
; APPLICANT: Nagamine, Kentaro
; TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN
; FILE REFERENCE: 11283-004001 US/09/600,087
; CURRENT APPLICATION NUMBER: 2000-07-11
; PRIOR APPLICATION NUMBER: PCT/JP99/06289

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/ PRIOR FILING DATE: 1999-11-11
/ PRIOR APPLICATION NUMBER: JP/321200/1998
/ PRIOR FILING DATE: 1998-11-12
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 2
/ TYPE: PRT
/ LENGTH: 1503
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: TRANSMEM
/ LOCATION: (320)...(344)
/ NAME/KEY: TRANSMEM
/ LOCATION: (750)...(773)
/ NAME/KEY: TRANSMEM
/ LOCATION: (794)...(818)
/ NAME/KEY: TRANSMEM
/ LOCATION: (867)...(891)
/ NAME/KEY: TRANSMEM
/ LOCATION: (900)...(924)
/ NAME/KEY: TRANSMEM
/ LOCATION: (932)...(956)
/ NAME/KEY: TRANSMEM
/ LOCATION: (1024)...(1048)
/ US-09-600-087-2

Query Match
Best Local Similarity 33.5%; Score 2039; DB 4; Length 1503;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

Qy 26 GEVNFSGGKRGKRVVPSPGVAPSLFDLLAEWHLPAPNLVSLVSGEOPFAMKSWLR 85
Db 128 GDVFTGLSQKVKYVRVSDTPSPSVIYHMTQHWGLDVPNLLISVTGAKNFKNPKLK 187
Qy 86 DVLKGLVKAQSTGAWILTSALRVGLARHVQOAVRDHSLASTSTKVRVAVGMSLGRV 145
Db 188 SIFRGLVKVQATQTAIIITGSHTVGMVKVGEAVRDFSLSSYKEGELITIGVATWGTV 247
Qy 146 LHRRLLEBAQEDFPVHYPPDDGGSGPLCLSDLSNLSHFILVPGPPGKGDGLTELRLE 205
Db 248 HRREGLIHTGSPFAEYILDENG-QGNLTCLDSNHSFILVDDGHGQYGVIEPIRLTLE 306
Qy 206 KHISQAGYGTGSIPIVLCLLVNGDPNLTISRVAEQAAPWLLILVSGSGIADVLAA 265
Db 307 KFISQTKERGCV-AIKPIVCVLEGGPGTLHTIDNATNGTFCVVGSGRVADVIAQ 365
Qy 266 LVNQP--HLLVPKVAEQ--FKEKFPKSHSWEDIVRWTKLQNIHQHLLTVYDPEQ 320
Db 366 VANLPVSDITSLIQKLSVFFQEMFET--FTESRIVEWTKIQDIVRRQLLTVFREGK 423
Qy 321 EGSEBLDTVILKALVKACKSHSQBPQDYLD-ELKLAVANDRVDIAKSEIFNGDVEWMSCD 379
Db 424 DQQQDVDAIIQALLKASRSQDHGHNWDHQLKLVANWNRVDIARSEIFMDEWQWPKSD 483
Qy 380 LEEVNDVALNKKPEFVRLFDVNGADVADFLTYGRQLQELYSVRKSLFLFDLLQKQBEA 439
Db 484 LHPTWTAALISNKPFEVFLFLENGVQLKEFVTWDTLLYENLDPSCFLSHSKLQK---- 538
Qy 440 RLTLAGLTQARPPAPG--PAPSLHEVSVLKDPLQDACRGFYQDGRPDRRR----- 492
Db 539 -----VLVDEPERPACAPAPRIQMHVAVQLVRELLGDFTQPLYPRPHNDRLLPLPV 592
Qy 493 -----AEKGPAPKPTQKQLLDLQNKSEPNRDLFLWAVLQNRHEMATYFWAMQO 542
Db 593 PHVKLVNQGVSRLSLYKSSGHVTF-----TMDPIRDLIIAIVQNRRELIGIWAQSO 646
Qy 543 EGVAALAAACILKEMSHLETAAR---ATRAKYERIALDLFSSCYNSSEARAPALL 599
Db 647 DCIAAALACSKILKELSKBEDTDSSEMLALAE-EYEHRAIGVFTCYRDEERAQKLL 705
Qy 600 VRRNRCKSTTCLHLATEADAKAPFAHDGVQAFTRIWMGDMAGTPIILRLGAFCLPAL 659
Db 706 TRUSEANGKTTCLQALEAKDMKVSHGIGTQAFITKVKVQGLSVNDGLWRVTLCLMAFPL 765

US-09-949-016-6341
US-09-949-016-6341
; Sequence 6341, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCES: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6341
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6341

Query Match
Best Local Similarity 33.5%; Score 2039; DB 4; Length 1503;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

Qy 26 GEVNFSGGKRGKRVVPSPGVAPSLFDLLAEWHLPAPNLVSLVSGEOPFAMKSWLR 85
Db 128 GDVFTGLSQKVKYVRVSDTPSPSVIYHMTQHWGLDVPNLLISVTGAKNFKNPKLK 187
Qy 86 DVLKGLVKAQSTGAWILTSALRVGLARHVQOAVRDHSLASTSTKVRVAVGMSLGRV 145
Db 188 SIFRGLVKVQATQTAIIITGSHTVGMVKVGEAVRDFSLSSYKEGELITIGVATWGTV 247
Qy 146 LHRRLLEBAQEDFPVHYPPDDGGSGPLCLSDLSNLSHFILVPGPPGKGDGLTELRLE 205
Db 248 HRREGLIHTGSPFAEYILDENG-QGNLTCLDSNHSFILVDDGHGQYGVIEPIRLTLE 306
Qy 206 KHISQAGYGTGSIPIVLCLLVNGDPNLTISRVAEQAAPWLLILVSGSGIADVLAA 265
Db 307 KFISQTKERGCV-AIKPIVCVLEGGPGTLHTIDNATNGTFCVVGSGRVADVIAQ 365
Qy 266 LVNQP--HLLVPKVAEQ--FKEKFPKSHSWEDIVRWTKLQNIHQHLLTVYDPEQ 320
Db 366 VANLPVSDITSLIQKLSVFFQEMFET--FTESRIVEWTKIQDIVRRQLLTVFREGK 423
Qy 321 EGSEBLDTVILKALVKACKSHSQBPQDYLD-ELKLAVANDRVDIAKSEIFNGDVEWMSCD 379
Db 424 DQQQDVDAIIQALLKASRSQDHGHNWDHQLKLVANWNRVDIARSEIFMDEWQWPKSD 483
Qy 380 LEEVNDVALNKKPEFVRLFDVNGADVADFLTYGRQLQELYSVRKSLFLFDLLQKQBEA 439
Db 484 LHPTWTAALISNKPFEVFLFLENGVQLKEFVTWDTLLYENLDPSCFLSHSKLQK---- 538
Qy 440 RLTLAGLTQARPPAPG--PAPSLHEVSVLKDPLQDACRGFYQDGRPDRRR----- 492
Db 539 -----VLVDEPERPACAPAPRIQMHVAVQLVRELLGDFTQPLYPRPHNDRLLPLPV 592
Qy 493 -----AEKGPAPKPTQKQLLDLQNKSEPNRDLFLWAVLQNRHEMATYFWAMQO 542
Db 593 PHVKLVNQGVSRLSLYKSSGHVTF-----TMDPIRDLIIAIVQNRRELIGIWAQSO 646
Qy 543 EGVAALAAACILKEMSHLETAAR---ATRAKYERIALDLFSSCYNSSEARAPALL 599
Db 647 DCIAAALACSKILKELSKBEDTDSSEMLALAE-EYEHRAIGVFTCYRDEERAQKLL 705
Qy 600 VRRNRCKSTTCLHLATEADAKAPFAHDGVQAFTRIWMGDMAGTPIILRLGAFCLPAL 659
Db 706 TRUSEANGKTTCLQALEAKDMKVSHGIGTQAFITKVKVQGLSVNDGLWRVTLCLMAFPL 765
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Db 188 SIFRGLVKVAQTTCGAWIITGSGHTGMVKQGEAVRDFSLSSYKEGELLITIGVATGCTV 247
Qy 146 LHRRILEAQBDFPHYEDDGGSGPLCSLDSNLSHFIYEPGPGKDGTELRLRL 205
Db 248 HRREGLIHPTGSPFAEYILDEG-QCNLTCLDSNLSHFIYEDDGHGQYVEIPURTRLE 306
Qy 206 KHISORAGYGTGIEIPVCLLVNGDPNTERISRAVEQAAPMLIIVGSGGIADVLAA 265
Db 307 KFISQTKERGV-AIKPIVCVILEGGEGTILHTDNTATNGTGPCVVEGSGRADVIAQ 365
Qy 266 LVNQP--HLLVPKVAEKQ---FKKFPKSHFWMEDIVRWTKLLQNTSHQHLITVYDEQ 320
Db 366 VANLPVSDITISLIQKLSVFQEMFET--FTESRIVEWTKKIQIDVRRRLITVREBK 423
Qy 321 EGSEELDTVILKALVAKSHSQEPDYL-D-ELKAVAWDRVDIAKSEIFNGDVKWCD 379
Db 424 DQOQDVDAILOALLKASRSQDFHGENWDHQLKAVAMNRVDIARSEIFMDEWOKPSD 483
Qy 380 LEEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYRSVRKSLFLDILLQKBEA 439
Db 484 LHPTTAALISNKPEFVKFLFENGVLQKEFVTDWTLTYLYENLDPSCLFHSKLOK----- 538
Qy 440 RLTLAGLGTQOAREPPAGE--PAFSLHVSRLVKDFLODACRGFYODGPGDRRR----- 492
Db 539 -----VLVEDPERPACAPAPLQMHVAQVLRLLGDTQPLYPHPRHNDRLRLLPV 592
Qy 493 -----AEKGPAPKRTGQKWLIDLNQKSENPRDLFLWAVLQNRHEMATIYFAMQO 542
Db 593 PHVKLVNQVSLRSYKRSGHVTF-----TMDPIRDLIIWAIQNRRELAGIWAQSQ 646
Qy 543 EGVAAALACKILKEMSHLETEAAR--ATREAKYERLALDLFSECSNSGEARAFALL 599
Db 647 DCTAALACSKILKELSGEEDTDSSEMLALAE-EYEHRAIGVFTCYRKEDEARQALL 705
Qy 600 VRNRCSWTKTLHLATEADAKAFFAHGQVQAFPLTRIMWGMMAAGTPILRLGAFICPAL 659
Db 706 TRVSEANGTKTCLQALEAKMKFVSHGGIQAFLTKVMWGSLVDNGLWRTVLCMLAFPL 765
Qy 660 VYTNLITFSEAPLRTGLELDQLDLSLDEKSPLYGLQSRVELVAPRAQDGRPAVF 719
Db 766 LLTGLISFREKR-----LQD-----VGTAA----- 786
Qy 720 LLTRWKFAGPVTYVFLGNVVMVFAFLFTYVLLVDPRPPGSGPEVLYFWVFTLV 779
Db 787 ---RARAFFTAPVYFHLNLTYSFAFLCLFAYILMVDQPV---PSWCECAIYMLFSLV 840
Qy 780 LEEIROGFFTDETHLVKKTLLVYGDNNKCDMVAFPLFTVGVTCMLPSAFAGRTVLA 839
Db 841 CEEMRQFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900
Qy 840 MDPVFTLRLIHIPAIHKQGPKIIVVERMKDVFFFLFSLVWLVAYGVTTOALLPHPD 899
Db 901 LDFILFCLRLMHIFTISKTLGPKIIVKRMKDVFFFLFLLAVVWVSGVAKQAILIHE 960
Qy 900 GRLEWIFRRLVRYLOIFQGP--LDEIDARVNC--THPLLEDSDSCPS----- 948
Db 961 RRVDMFRGAVYHSLYITFGIPIGVIDGVNFNPEHCSPNGTDPY-----KPKCESDAQO 1016
Qy 949 --LYANWLVILLVTLVTLNVLMLNLLIAMFSYTFQVQGNADMFWKFORNYLVSYHE 1006
Db 1017 RPAPEPWLTVLLCLYLTLNLLNLLIAMFNITFOQVHEHTDQIWKFORHDLIEYHG 1076
Qy 1007 RPALAPFPFILLSHLSLTLRRVFKKEAEHREHLERDLPDLDQKVVVTWETVQKENFLSKM 1066
Db 1077 RPAAPPFILLSHLQLFKRVVLTAKRHKQKLNKLEKNEEAALLSWEIYKENVLQNR 1136
Qy 1067 EKRDRSEGEVLRTAHRVDPIAKYL-----GGLREQKR1KCLSEINYSVLVSS 1118
Db 1137 QFOQKREPEQKIEDISNKVDAMVDLLDLDPLKRSISM---EORLASLEEQAQATARALHW 1193
Qy 1119 VADVLQAQGGPRSSQHCCEGSQLVAD---HRGGLDGWEQPG 1157
Db 1194 IVTRLASGFSSEADVPVTLASQKAAEBPDAEPGGRKKTTEEPG 1235

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RESULT 6

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US-09-112-096-15
; Sequence 15, Application US/09112096
; Patent No. 6194152
; GENERAL INFORMATION:
; APPLICANT: Reiner Laus
; APPLICANT: Michael H. Shapiro
; APPLICANT: Larisa Tsavaler
; TITLE OF INVENTION: Prostate Tumor Polynucleotide and
; TITLE OF INVENTION: Antigen Compositions
; FILE REFERENCE: 7636-0015.30
; CURRENT APPLICATION NUMBER: US/09/112.096
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: 60/056.110
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-112-096-15

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Query Match      25.7%; Score 1566.5; DB 3; Length 1095;
Best Local Similarity 34.3%; Pred. No. 3.9e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

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Qy 26 GEVPPGGSGKRGKVRVPSPVAPSVLPDILLAEWHLPAPNLVSLVSGEOPPFAMKSLR 85
Db 95 GDIPETLGGK-GKYIRLSCDTDAEILYELLTQHWHLKTPNLVLSVSGAKNFALKPRMR 153
Qy 86 DVLKGLVAKAAGTCGAWILTSALRYGLARHVGQAVRDHSLASTSTKRVAVGMAASLGRV 145
Db 154 KIFSR-LYIAOSKGAWILTGTHYGLTKYIGEVRDNTI-SRSEENIYALGIAANGV 211
Qy 146 LHRRILE---EAQEDFPVHYPPDDGGSGQPLCSLDSNLSHFIYEPGPGKDGTELRL 202
Db 212 SNRDTLIRNCDAEGYFLAQLMDD--FTRDPLVILDNHNLHLLVDNGCHGHPVTEAKLN 270
Qy 203 RLEKHISE---ORAGYGTGSGTIEIPVCLLVNGDPNTERISRAVEQAAPMLIIVGSGGI 259
Db 271 QLEKHISERTIQDSNYG---KIPVCPAQGGKGTILKAINTSIKNKIPCVVVEGSGRI 326
Qy 260 ADVLAALVNPQLLVPKVAEKQFKEKFS--KHFWSMEDIVRWTKLLQNTSHQHLITVYD 317
Db 327 ADVIASLVEVEDAPTSSAVKEKLVRFPLPRTVSRLESEETESIKWLEKLECSHLLTVIK 386
Qy 318 FQEGSEELDTVILKALVAKSHSQEPDYLDELKLA VAWDRVDIAKSEIENGVDVWKS 377
Db 387 MEEAGDEIVSNALSYALYKAFSTSEQDKDNWNGQLKLLLEWQLDLANDEIFTNDRRWS 446
Qy 378 CDLEEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYRSVRKSLFLDILQ---R 434
Db 447 ADLQEVWFTALIKDRKPFVRLFLEGNLNRKELTHDVLTELF--SNHFSLTVRNLQIAKN 505
Qy 435 KQSEARLTLAGLGTQOAREPPAGPAPFSLHVSRLVKDFLODACRGFYODGPRG--DRRA 493
Db 506 SYNDALLTF-----VWKLVANFR-----RGFRKREDNRGRDMDI 539
Qy 494 EKGPAKRTGQKWLIDLNQKSENPRDLFLWAVLQNRHEMATIYFAMQOEGVAAALAAACK 553
Db 540 E-----LHDVSPITRHPLQALFIWAILQNKLSKVIVETQCTGCTLAALGASK 587
Qy 554 ILKEMSHLETEAARATREA--KYERLALDLFSECSNSGEARAFALLVRNRNCWKTTC 611
Db 588 LKTLAKVNDINAAGESEELANEYETRAVELFTECYSSDEDLAEQLLVYSCWAGGSGNC 647
Qy 612 LHATEADAKAFPAHDGVQAFPLTRIMWGMMAAGTPILRLGAFICPALVYTNLITFSEA 671
Db 648 LELAVEATDQHTAQPGVQNFSLSKQWYGEISRDTKNWKIILCLFIPLVCGGFSFRKK- 706

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Db 1071 HRFRQDLDKLNKGLLKEIANKIK 1095

RESULT 8

US-09-685-166A-778

Sequence 778, Application US/09685166A

Patent No. 6630305

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John H.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C21

CURRENT APPLICATION NUMBER: US/09/685,166A

NUMBER OF SEQ ID NOS: 898

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 778

LENGTH: 1095

TYPE: PRN

ORGANISM: Homo sapiens

US-09-685-166A-778

Query Match 25.7%; Score 1566.5; DB 4; Length 1095;

Best Local Similarity 34.3%; Pred. No. 3.9e-144;

Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

Qy 26 GEVFGGSKGKGFVRVPSGVAPSVLPDLLAEHLPAPNLVSVISLAGEOPFAMKSWLR 85

Db 95 GDIQFETUGK-KGYIRLSCOTDAEILYELLTQHWHLTPNLVISTGKAKNFALKPRMR 153

Qy 86 DVLRLKGLVKAOSTGAWILTSALRVLGRVQAVRDHSLASTSTKRVVAVGMASLGRV 145

Db 154 KIFSR-LIYIAQSKGAWILTGTHYGLTYIGEVRDNTI-SRSSEENIVAIGIAWGV 211

Qy 146 LHRRIE---EAQEDFPVHPEDDGGSGPLCSLNSHFLIVBPFGPKDGLTELRL 202

Db 212 SNRDTLRNCDAEGYFLAQLMDD-PTRDPLYLDNNHLLLVONGCHGCHPTVEAKLRN 270

Qy 203 RLEKHISE---QVAGGCTGSTEIPVCLLVNGDPNLTIERISRAVEQAAPWLLVSGGI 259

Db 271 QLEKHTISERTIODNSYQ---KIPIVCPAQGGKTELKAIINTSIKNIKPCVWVSGGRI 326

Qy 260 ADVLAALVNQPHLLVPKVAEKOPKEKPPS--KHFSWEDIVRWTKLQNTISHOHLITVYD 317

Db 327 ADVIASLVEVEDAPTSASVAKELVRLPRTVSRLSSEETESWKWLKEILECSHLLTVIK 386

Qy 318 FEQEGSEELDTVLKALVKACKSHSQEPQDYLDLKLAVAWDRVDIAKSEIFNGDVWES 377

Db 387 MEEAGDEIVSNALSYALKAFSTSEQDKNNWQQLKLEWNLQDLANDEIFTNDRWES 446

Qy 378 CDLEEVWMDALVNKBEFVLFLVDNGADVADFLTYGLYELQELYSVSRKSLFLDQLQ---R 434

Db 447 ADLQEVMTALIKDRPKFLEFLNLGLNRKFLTHDVLTELP-SNHFTLVYRNLOIAKN 505

Qy 435 KQEARLTLAGLGTQQAAREPPAGPAPFSLHEVSRVLKDLQDACRGFYQDGRPG-DRRRA 493

Db 506 SYNDALLTF-----VWKLVANFR-----RGRKEDRNGRDEMIDI 539

Qy 494 EKGPAPKPTGQKWLDDLNQKSENPRWDLFLWAVLQNRHEMATYFWAMQBGVGAALAAACK 553

Db 540 E-----LHDVSPITRHPQLQALFWAILQNKELSKVITWQTRGCTTAAALGASK 587

Qy 554 ILKEMSHLETEAEARATREA--KYERLALDLSECYNSSEARAFALLVVRNRCWSKTTTC 611

Db 588 LLKTLAKVNDINAAGESEELANEYETRAVELTECYSSDEDLAEQLLVVSCAENGSGNC 647

Qy 612 LHLATEADAKAFPAHGDVQAFLTRIMWGDMAAGPILRLGCAFLCPALVTNLTITFSEE 671

Db 648 LELAPEATDQFTRAPGVQNFSLSKQWGEISRDTKWKKIILCLFIIPLVGCGFVSFRKK- 706

Qy 672 PLRTGLEDLQDLSLDTKSPLYGLQSRVBELEAPRAQGRGPRAVFLTRMKKFWGAP 731

Db 707 -----PVDKHKK-----LLWYVVAFTSP 725

Qy 732 VTFLGNVVMYFAFLFTVYLLVDPRPPGPGSPGVFTLYFWVFTLVLEIRIOGFFTDE 791

Db 726 FVFSMNWVFYIAFLLLFAYLLMDFHSVPH---PPELVLYSLVFLVPCDEVROWVNGV 782

Qy 792 DTHLVKKFTLYVGNWKNKCDMVAIFLFIIVGVTCRM---LPSAFBAGRTVLAMDPMVFTLR 848

Db 783 N-----YFTDLNVMMDTLGLFYFIAGIVFRLHSNKSLSYSGRVIFCLDIIFTLR 833

Qy 849 LIHIFAIHKOLGPKIIVVERMKDVFFFLFSLVMLVAYGVTTQALLHPHGRLEWIPRR 908

Db 834 LIHIFTVSRNLGPKIIMLQMLIDVFFFLFLFAVWVAFVARGQILRQNRWRWIFRS 893

Qy 909 VLYRPYLIQFQIPLDEIDEAR---VNCS-----THPLLE-DSPSCPSLYANWLVILL 959

Db 894 VIYEPYLAHQVPSD-VDGTTYDFAHCTFTGNSKPLCVLDEHNLPR-FPEWITITPLV 951

Qy 960 VTFLLVNTVLLMILLIAMESYTFQVQGNADMFKFORYNLIVYHERPALAPPILLSH 1019

Db 952 CIYMLSTNILLVNLVAMFGYTVGTQENNDQVWKFQYFLVQVYCSRLNIPFFPIVAY 1011

Qy 1020 LSLTRVRFVKEAEHREHLERDLDPDLDQKVVTWETVQKFNFLSKMEKRDRDSGEVLR 1079

Db 1012 PYMVVKCKFCCKCKEKNMESSVCCFKNEDNETLAWGVWKNYLVKINTKANDT-SEEMR 1070

Qy 1080 KTAHRVDPIAKYLG-LREQEKRIK 1103

Db 1071 HRFRQDLDKLNKGLLKEIANKIK 1095

RESULT 9

US-09-679-426-778

Sequence 778, Application US/09679426

Patent No. 6759515

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

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APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C20

CURRENT APPLICATION NUMBER: US/09/679,426

CURRENT FILING DATE: 2000-10-02

Db 327 ADVIASLVEDEAPTSSAVKEKLVRLPRTVSRLESEETESWIKWLKEILSCSHLLTVIK 386
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Db 387 MEEAGDEIVSNAISYALYKAFSTSEQDKNWNGQKLLLEWNLQDLANDEIFTNDRWES 446
Qy 378 CDLEBVMVDALVSNKPEFVRLFDVNGADVFLTYGRLOELYSRSRKSLLFDLLQ---R 434
Db 447 ADLQEVMTALIKDRPKFVRLFLENGNLKRLKFLTHDVLTELF-SNHFTLVYRNLIQAKN 505
Qy 435 KOSEARLTLAGLGTQOAREPPAGPPAFSLHVEVSRLVKDFLOQACRGFYQDGRPG-DRRRA 493
Db 506 SYNDALLTF-----VKLVANFR-----RGFRKEDRNGDEMNDI 539
Qy 494 EKGPAKRTGQKWLIDLQKSNPWRDLFLWAVLQNRHEMATYFWAMQEGVAAALACK 553
Db 540 E-----LHDVSPITRHPLOALFIWAILQNKKLSKVWIEQTRGCTLAALGASK 587
Qy 554 ILKEMSHLETEAARATREA--KYERLALDLFSECYSNSEARAFALLVRNRNCWSKTTC 611
Db 588 LKTLAKVNDINAAGESEELANEYETRAVELFTECYSDDEDLAQLLVYSCAAGGSGNC 647
Qy 612 LHLATEADAKAFFAHDGVOAFLTRIWMGDMAGTPIRLGLAFGLCPALVYTNLITFSEBA 671
Db 648 LELAVEATDQHFTAQPGVQNFSLKQWYGEISRDITKNWIKILCLFIIPLVGCGFVSFRKK- 706
Qy 672 PLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQDGRGPRAVELLTWRKFWGAP 731
Db 707 -----PVDKHKK-----LLWYVAFFTSP 725
Qy 732 VTVELGNVMYFAELFLTYVLLVDFRPPPGQSPGPEVTLVFWVTLVLEIRQCGFFTDE 791
Db 726 FVFSWNVVYFAELFLTYVLLVDFRPPPGQSPGPEVTLVFWVTLVLEIRQCGFFTDE 782
Qy 792 DTHLVKFTLYYQDNWKNKCDMVAIFLIVGVTCRM---LPSAFEAGRTVLAMDFVFTLR 848
Db 783 N-----YFTDLNWNMDTLGLFVFIAGIIVFRLHSSNKSLSYSGRVIFCLDIIFTLR 833
Qy 849 LHIHFAHKQKGIIVERMKNQVFFLFLSVMLVAVGVTTOALLHHPDGLRWIFRR 908
Db 834 LHIHFTVSNLGPKIIMLQMLIDVFFFLFPAVMVAFVQARQIGLRQNEQRWIFRS 893
Qy 909 VLRYRVLQIPGOIPLEIDEAR---VNCS-----THPLLE-DSPSCPSLVANMLVILIL 959
Db 894 VIEPYLAMPQVPSD-VDGTVDFAHCTFTGNEKPLCVLDELHMLPR-FPEWITPLV 951
Qy 960 VTFLLVTVNLLMMLIAMFSYTFQVVGQNMDFWKFQRYNLIVEXHERPALAPPPFILLSH 1019
Db 952 CIYMLSTNILLNVLVAMFGYTVGTQENNDQWKFQRYFLVQYCSRLNIPFPFIVFAY 1011
Qy 1020 LSLTLRRVPKKEAHKREHLERDLDPDLOQKVVTWETVOKENFLSKMEKRRDSEGEVL 1079
Db 1012 FYMWVKKCFKCCCKEKNMSESSVCCPNEDNETLANEGVMKENYLVKINTKANDT-SEENR 1070
Qy 1080 KTAHRVDFTAKYLG-LREQEKIK 1103
Db 1071 HRFRQDLTKLNDLKLKSIANKIK 1095

RESULT 11
US-09-651-236-778
; Sequence 778, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651.236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 778
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-651-236-778

Query Match 25.7%; Score 1566.5; DB 4; Length 1095;
Best Local Similarity 34.3%; Pred. No. 3.9e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

Qy 26 GEVNFSGGKRGKRVPSGVAPSVLPDLLAEWHLPAPNLVSVLSVGBEOPFFAMKSWLR 85
Db 95 GDIQFETLGKK-GKIVRLSCDTPDAEILLYELLTQHWHLKTPNLVSVTGGAKNFALKPRMR 153
Qy 86 DVLAKGLVKAQSTGAMILTSALRVGLARHVQAVRHSLASTSTKVRVAVGASLGRV 145
Db 154 KIFSR-LIYIAQSKGAWILTGTHYGLTKYGEVVRDNTI-SRSEENIVAIGIAWGMV 211
Qy 146 LHRRLTLE---EAQEDFPVHYPPEDDGGSGQGLSDLSNLSHFLVPEPPGPGDGLTELRL 202
Db 212 SNRDTLRNCDAEGYFLAQYLMDD-FTRDPLYLDNNHLLHLLVDNGCHGHTPTVEAKLRN 270
Qy 203 RLEKHISB---QAGYGGTGSIEIPVCLLVNGDPNTLERISRAVEQAAPMLILVSGGI 259
Db 271 QLEKHISERTQDSNYG---KIPVCAQGGKGTIKAINTSIKNKIPCVVVEGSGRI 326
Qy 260 ADVLAALVNPQHLVPRVAEKQFKEKFP--KHSWEDIIVRTWKLQNLQITSHOHLITVYD 317
Db 327 ADVIASLVEDEAPTSSAVKEKLVRLPRTVSRLESEETESWIKWLKEILSCSHLLTVIK 386
Qy 318 FEQGESELDVTILKALVKACKSHSQBPQDYLDELKAVANDRVIAKSEIFNGDVEWKS 377
Db 387 MEEAGDEIVSNAISYALYKAFSTSEQDKNWNGQKLLLEWNLQDLANDEIFTNDRWES 446
Qy 378 CDLEBVMVDALVSNKPEFVRLFDVNGADVFLTYGRLOELYSRSRKSLLFDLLQ---R 434
Db 447 ADLQEVMTALIKDRPKFVRLFLENGNLKRLKFLTHDVLTELF-SNHFTLVYRNLIQAKN 505
Qy 435 KOSEARLTLAGLGTQOAREPPAGPPAFSLHVEVSRLVKDFLOQACRGFYQDGRPG-DRRRA 493
Db 506 SYNDALLTF-----VKLVANFR-----RGFRKEDRNGDEMNDI 539
Qy 494 EKGPAKRTGQKWLIDLQKSNPWRDLFLWAVLQNRHEMATYFWAMQEGVAAALACK 553
Db 540 E-----LHDVSPITRHPLOALFIWAILQNKKLSKVWIEQTRGCTLAALGASK 587
Qy 554 ILKEMSHLETEAARATREA--KYERLALDLFSECYSNSEARAFALLVRNRNCWSKTTC 611
Db 588 LKTLAKVNDINAAGESEELANEYETRAVELFTECYSDDEDLAQLLVYSCAAGGSGNC 647
Qy 612 LHLATEADAKAFFAHDGVOAFLTRIWMGDMAGTPIRLGLAFGLCPALVYTNLITFSEBA 671
Db 648 LELAVEATDQHFTAQPGVQNFSLKQWYGEISRDITKNWIKILCLFIIPLVGCGFVSFRKK- 706
Qy 672 PLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQDGRGPRAVELLTWRKFWGAP 731
Db 707 -----PVDKHKK-----LLWYVAFFTSP 725


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QY 732 VTFLGNVVMYFAELFTYVLLVDPRPPPOGSPGPEVTLYFWVFTLVLEIRQGFTE 791
Db 726 FVFSNMVVFYIAFLLLFAYLLMDPHSVPH---PPELVLYSLVFLVFCDEVRQWYVNCV 782
QY 792 DTHLVKKTLVYGNWNNKCDMAIFLPIVGTCTCM---LPSAFAAGRTVLAMDFMVFTLR 848
Db 783 N-----YFTDLNVMNMDLGLFYFIAGIVFRLHSSKSSLYSGRVIFCLDYIIFTLR 833
QY 849 LIHIFAIHKOIQLPQKIIIVVERMKDVFFLFLSVLWVAYGVTTQALLHHPDGRLEWIFRR 908
Db 834 LIHIFTVSRNLGPKIIMLQRMIDVFFFLFAVMVAFVAGQGLRQNRWIFRS 893
QY 909 VLYEPYLIQFGOIPLDIDBEAR---VNCS-----THPLLE-DSPSCPSLYANWLVILL 959
Db 894 VIYEPYLAAMFGQVPSD-VDGTYYDFAHCTFTGNEKFLCVELDEHNLPR-FPEWITPLV 951
QY 960 VTFLVTVNLLMILLAMSYTFQVQGNADMFQFQRYNLIYEHYERPALAPPFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTQENNDQWKFQRYFLVQVYCSRLNIPFPFIVFAY 1011
QY 1020 LSLTLRVFKKEAHEHREHLERDLPDLPDQKVVVWTVOKENFLSKMEKRRRDSGEVLR 1079
Db 1012 FYMVVKKCFKCCCKEKNWESSVCCPKEDNETLAWGVKYNLVKINTKANDT-SEEMR 1070
QY 1080 KTAHRVDFTAKYLG-LRQEKRIK 1103
Db 1071 HRFRQDVTKLDLKGLLAEIANIK 1095

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RESULT 12

US-09-636-215-780

Sequence 780, Application US/09636215

Patent No. 6620922

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, David C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqi
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.42717C17

CURRENT APPLICATION NUMBER: US/09/636,215

NUMBER OF SEQ ID NOS: 852

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 780

LENGTH: 1095

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(1095)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-636-215-780

Query Match 25.6%; Score 1558.5; DB 4; Length 1095;
 Best Local Similarity 34.1%; Pred. No. 2.4e-143;
 Matches 377; Conservative 203; Mismatches 394; Indels 131; Gaps 27;
 26 GEVNFSGGKKRKFVRVPSGVAPSVLPDLLLAHNLPAVNLVSLVCEQPFAMKSWLR 85

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Db 95 GDIOFETLGGK-KGIRISCDTDAEILYELLTQHWHLKTPNLNLVSVTGGAKNFAKPRMR 153
QY 86 DVLKGLVKAAGSTGAWILTSAIRVGLARHVGQAVROHSLASTSTKRVVAVGASLGRV 145
Db 154 KIFSR-LIVIAQSKGAWILTGTHVGLMKYIGEVVRDNTI-SRSSEENIVAIIGAAWGV 211
QY 146 LHRRIIE---EAQEDFPVHYPEDGGGQPLCSLDSNLSHFILVFERPPGKGDLTELR 202
Db 212 SNRDTLIRNCDAEGVFLAQLMDD-FTRDPLYLIDNNHTLLLDVNGCHGHPVTEAKLN 270
QY 203 RLEKHISE---ORAGYGTGOSIEIPVLCILVNGDPNLTBRISRAVQAAPWLLVSGGI 259
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QY 260 ADVLAALVNPHLLVPAKVKQPKKFPF---KHFSWEDIVRWTKLLQNTSHQHLITVVD 317
Db 327 ADVIASLVEDELTSAVKEKLVRFPLRTVSRLEPEETESIKWLKEILECSHLLTVIK 386
QY 318 FEQSGSELDVTILKALVKACKSHSQEPQDYLDLKLAVANDRVDIKSEIFNGDVWKS 377
Db 387 MEEAGDSIVSNAISYALYKAFSTSEQDKDNWNGQLKLLLEWNLQDLANDEIFTNDRWES 446
QY 378 CDLEEVMVDALVSNKPEFVRLFVDNCAVDALTYGRLOELYSRVSRLFLDLQ---R 434
Db 447 ADLQEVMTALIKDRPKFVRLFENGLNLRKPLTHDVLTELF-SNHFTSLVYRNLIQAKN 505
QY 435 KQEEARLTLAGLTQOAREPPAGPPAFSLHEVSRVLKDFLQDACRGFFVQDRPG-DRRA 493
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QY 494 EKGPAKRPTGQKWLDDLKOKSENPMRDLFVAVLONRHEMATYFWAMQBGVAAAALAA 553
Db 540 E-----LHDVSPITRHPLOALFIWAILONKELSKVITWETRGTCTLAALGASK 587
QY 554 ILKEMSHLETEARARATREA---KYERLALDLSECYNSSEARAFALLVRNRCWKTTC 611
Db 588 LLKTLAKVKNIDINAGSEBELANEYETRAVELTECYSSDEDLAEQLLYVSCAMGSGNC 647
QY 612 LHLATEADAKAFFAHDGVQAPLTVRIWMDMAACTPILRLGAPLCPALVYTNLIITFSEA 671
Db 648 LELAVEATDQHFIAQPGVQNFSLQWVGEISRTKNWIKILCLFIPLVCGCFVFRKK- 706
QY 672 PLRTGLEDLQDLSLDEKSPLYGLOSERVEELVEAPRAQGRGPRAVFLLTWRKFWGAP 731
Db 707 -----FVDKHKK-----LLWYVAFPTSP 725
QY 732 VTFLGNVVMYFAFLFTYVLLVDPRPPPOGSPGPEVTLYFWVFTLVLEIRQGFTE 791
Db 726 FVFSNMVVFYIAFLLLFAYLLMDPHSVPH---PPELVLYSLVFLVFCDEVRQWYVNCV 782
QY 792 DTHLVKKTLVYGNWNNKCDMAIFLPIVGTCTCM---LPSAFAAGRTVLAMDFMVFTLR 848
Db 783 N-----YFTDLNVMNMDLGLFYFIAGIVFRLHSSKSSLYSGRVIFCLDYIIFTLR 833
QY 849 LIHIFAIHKOIQLPQKIIIVVERMKDVFFLFLSVLWVAYGVTTQALLHHPDGRLEWIFRR 908
Db 834 LIHIFTVSRNLGPKIIMLQRMIDVFFFLFAVMVAFVAGQGLRQNRWIFRS 893
QY 909 VLYRPYLIQFGOIPLDIDBEAR---VNCS-----THPLLE-DSPSCPSLYANWLVILL 959
Db 894 VIYEPYLAAMFGQVPSD-VDGTYYDFAHCTFTGNEKFLCVELDEHNLPR-FPEWITPLV 951
QY 960 VTFLVTVNLLMILLAMSYTFQVQGNADMFQFQRYNLIYEHYERPALAPPFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTQENNDQWKFQRYFLVQVYCSRLNIPFPFIVFAY 1011
QY 1020 LSLTLRVFKKEAHEHREHLERDLPDLPDQKVVVWTVOKENFLSKMEKRRRDSGEVLR 1079
Db 1012 FYMVVKKCFKCCCKEKNWESSVCCPKEDNETLAWGVKYNLVKINTKANDT-SEEMR 1070
QY 1080 KTAHRVDFTAKYLG-LRQEKRIK 1103

```

Db 1071 HRFQDLTKLNDLKGLLKEIANKIK 1095

RESULT 13

US-09-685-166A-780

Sequence 780, Application US/09685166A

Patent No. 6630305

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

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APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C21

CURRENT APPLICATION NUMBER: US/09/685,166A

CURRENT FILING DATE: 2000-10-10

NUMBER OF SEQ ID NOS: 898

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 780

LENGTH: 1095

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(1095)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-685-166A-780

Query Match 25.6%; Score 1558.5; DB 4; Length 1095;

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Qy 26 GEVNFEGGKGGKGVVRVPSGVAPSVLFDLLAEHLAPNLVSLVSGEEQPFAMKMLR 85

Db 95 GDIQFETLGGK-GKYLSCDSDAEILYELLTQHHLKTPNLVSVTGGAKNFALKPRMR 153

Qy 86 DVLKGLVKAAQSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMASLGRV 145

Db 154 KIFSR-LIVIAQSGAWILTGTHYGLMKYIGEVVRDNTI-SRSSEENIVAIQIAWGMV 211

Qy 146 LHRRLTLE--EAGDPVHVPPDDGSGQGLCSLSDNLSHFLVPEPVPKGGDGLTELRL 202

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Db 271 QLEKYSERTIQDSNYGG---KIPVCAQGGKGTAKINTSIKNKIPCVVVEGSGGI 326

Qy 260 ADVLAALVNQPHLLVPKVAEKQPEKPPS--KHFSWEDIVRWTKLLQNTSHQLLTVDYD 317

Db 327 ADVIASLVEVEDALTSVAKEKLVRLPRTVSRLPPEETESWIKLKEILECSHLLTVTK 386

Qy 318 FEQEGSEELDTVLKALVKACKSHSQEPQDYLDELKLAVDWDVDTAKSEIFNGDVWES 377

Db 387 MEEAGDEIVSNALSYALYAFSTSEQDKNNWQGLKLLLENNQLDLANDEIFTNDRWES 446

Qy 378 CDLEEVVADALVNSKPEFVRLFDVNGADVADFTYGRLOELVRSVRKSLIFLLQ---R 434

Db 447 ADLQEVNFTALIKORPKFVRLFLENGLNRKFLTHDVLTFLP-SNHFSTLVYRNLIQAKN 505

Qy 435 KQBEARLTLAGLGTQOQAREPPAGPPAFPSLHEVSRVLKDFLODACRGYQDGRPG-DRRRA 493

Db 506 SYNDALLTF-----VWKLVANFR-----RGFRKEDRNGRDEMDI 539

Qy 494 EKGPAKPTQOKWLLDLNOKSENPRDLFLWAVLQNRHEMATYFWANGQEGVAAALAAACK 553

Db 540 E-----LHDVSPITRHPLOALFIAWLNQKKEISKVITWQTRGCTLAUAGASK 587

Qy 554 ILKEMSHLETEAARATREA--KYERLALDLFSECYNSSEARAFALLVRRNRCSWTKTC 611

Db 588 LLKTLAKVNDINDNAGESEELANEYETRAVELFTECYSSDEDLAEQLLVVSCAAGSGNC 647

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Db 707 -----PVDKHK-----LWYVVAFTTSP 725

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Db 726 FVFSWNVVFYIAFELLFAYVLLMDFSVPH---PPELVLYSLVFLVFCDEVQWYNGV 782

Qy 792 DTHLVKGFLLYVGNWNKCDMAIFLFIIVGVTCRM---LPSAFBAGRTVLAMDPMVFTLR 848

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Qy 909 VLYRPLYQIGQIPLDEIDEAR---VNCS-----THPLLE-DSPSCPSLVANMLVILL 959

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RESULT 14

US-09-679-426-780

Sequence 780, Application US/09679426

Patent No. 6759515

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Vedwick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

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, TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
, FILE REFERENCE: 210121.427C20
, CURRENT APPLICATION NUMBER: US/09/679,426
, CURRENT FILING DATE: 2000-10-02
, NUMBER OF SEQ ID NOS: 895
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 780
, LENGTH: 1095
, TYPE: PRT
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: VARIANT
, LOCATION: (1)...(1095)
, OTHER INFORMATION: Xaa = Any Amino Acid
US-09-679-426-780

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Best Local Similarity 34.1%: Pred. No.2.4e-143;
Matches 377; Conservative 203; Mismatches 394; Indels 131; Gaps 27;

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RESULT 15
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; Sequence 780, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1095)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-759-143-780

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203 RLEKHISE--CRAGYGGTSGSIEIPVLGLLVNGDPNTLIERISRAVEQAAPMLILVSGSGI 259
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260 ADVLAALVNQPHLLVPKVAOKFKKPPS--KHFSWEDIVRWTKLLQNLITSHOHLTLTYD 317
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)
2556.207 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1714042

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	6078	99.8	1167	16	US-10-794-897-2
5	6057.5	99.4	1164	9	US-09-834-792-5
6	5985	98.2	1165	16	US-10-794-897-7
7	5134.5	84.3	1168	16	US-10-794-897-8
8	5088.5	83.5	1158	9	US-09-834-792-2
9	5088.5	83.5	1158	13	US-10-026-188-5
10	5088.5	83.5	1158	16	US-10-794-897-4
11	5025.5	82.5	1156	16	US-10-794-897-6

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13	2448.5	40.2	1166	15	US-10-295-027-558	Sequence 558, App
14	2448.5	40.2	1166	15	US-10-295-027-916	Sequence 916, App
15	2448.5	40.2	1214	14	US-10-142-649-2	Sequence 2, Appli
16	2448.5	40.2	1214	17	US-10-789-378-80	Sequence 80, Appli
17	2448.5	40.2	1214	17	US-10-847-918-30	Sequence 30, Appli
18	2448.5	40.1	1214	15	US-10-343-114-10	Sequence 10, Appli
19	2428	39.8	1127	16	US-10-643-795A-123	Sequence 123, App
20	2428	39.8	1127	17	US-10-948-518-123	Sequence 123, App
21	2412.5	39.6	1129	15	US-10-391-399-2	Sequence 2, Appli
22	2353	38.6	1083	9	US-09-789-481C-2	Sequence 44, Appli
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29	2039	33.5	1503	16	US-10-467-163-3	Sequence 3, Appli
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44	1566.5	25.7	1095	14	US-10-144-678A-778	Sequence 778, App
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ALIGNMENTS

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; Sequence 8, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human ltrpc6
US-10-026-188-8

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QY 901 RLEWIFRVLRYPIQIFGQPLDEIDEARVNCSTHPLLEDSPCSLYANWLVILLV 960
Db 901 RLEWIFRVLRYPIQIFGQPLDEIDEARVNCSTHPLLEDSPCSLYANWLVILLV 960
QY 961 TFLVTNVLNMLLIAMSYTFQVQGNADMPKQRYNLIVEYHERPALAPPFILLSHL 1020
Db 961 TFLVTNVLNMLLIAMSYTFQVQGNADMPKQRYNLIVEYHERPALAPPFILLSHL 1020
QY 1021 SLTLRRVFKKAEHREHLRDLDPDQKVVTWETVQENFLSKMEKRRDSEGEVLK 1080
Db 1021 SLTLRRVFKKAEHREHLRDLDPDQKVVTWETVQENFLSKMEKRRDSEGEVLK 1080
QY 1081 TAHRVDFIAGLLEQEKRIKCLSQINCSVLSSVADVLAQGGGPRSSQCHGEGSQ 1140
Db 1081 TAHRVDFIAGLLEQEKRIKCLSQINCSVLSSVADVLAQGGGPRSSQCHGEGSQ 1140
QY 1141 LVAADHRCGLDQWPGAGQPPSDT 1165

Db 1141 LVAADHRCGLDQWPGAGQPPSDT 1165
RESULT 2
US-10-408-765A-1150
; Sequence 1150, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1150
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1150
Query Match 100.0%; Score 6093; DB 16; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQDVQGRPRPGSDAEDRRRELGLHRGEVNFVGGSGKRGKRVVPVSGVAPSLVFLDLLEAW 60
Db 1 MQDVQGRPRPGSDAEDRRRELGLHRGEVNFVGGSGKRGKRVVPVSGVAPSLVFLDLLEAW 60
QY 61 HLPAPNLVSLGEEOPFAMKSWLRLVLRGLVKAQSTGAWILTSALRVGLARHVQAV 120
Db 61 HLPAPNLVSLGEEOPFAMKSWLRLVLRGLVKAQSTGAWILTSALRVGLARHVQAV 120
QY 121 RDHSLASTSKVRVAVGASLGRVLRHRLLEAEQEDFFVHYPEDDGGSGQLCLSDSNL 180
Db 121 RDHSLASTSKVRVAVGASLGRVLRHRLLEAEQEDFFVHYPEDDGGSGQLCLSDSNL 180
QY 181 SHFILLVEPPGKDGTLRLRLKHLSEQRAGYGGTGSIEIPVLCLLVNGDPNTLRI 240
Db 181 SHFILLVEPPGKDGTLRLRLKHLSEQRAGYGGTGSIEIPVLCLLVNGDPNTLRI 240
QY 241 SRAVEQAAPWLLVSGGGIADVLALVNOPHLLVPKVAEKQPKFPPSKHFSWEDIVRWT 300
Db 241 SRAVEQAAPWLLVSGGGIADVLALVNOPHLLVPKVAEKQPKFPPSKHFSWEDIVRWT 300
QY 301 KLLQNTITSHQHLTVYDFEQSGSEELDTVLKALVKACKSHSQEPQDYLDLKLAVADR 360
Db 301 KLLQNTITSHQHLTVYDFEQSGSEELDTVLKALVKACKSHSQEPQDYLDLKLAVADR 360
QY 361 VDIKSEIFNGDVWKSCLLEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYL 420
Db 361 VDIKSEIFNGDVWKSCLLEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYL 420
QY 421 SVSRKSLFFDLQRKQEEARLTLAGLGTQAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
Db 421 SVSRKSLFFDLQRKQEEARLTLAGLGTQAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
QY 481 FYQDGRPGDRRRAEKGPAKPTGQKWLDLNOKSENPRDLFLMAVLQNRHEMATYFWAM 540
Db 481 FYQDGRPGDRRRAEKGPAKPTGQKWLDLNOKSENPRDLFLMAVLQNRHEMATYFWAM 540
QY 541 GQGVAAALAAACKILKEMSHLETEAARAATREAKYERLALDLFSECYSNSEARAFALLV 600
Db 541 GQGVAAALAAACKILKEMSHLETEAARAATREAKYERLALDLFSECYSNSEARAFALLV 600
QY 601 RNRCSKTTTCLHLATEADAKAFFAHGQVQAFLTRIWMGDMAGTPILRLGAFICPALV 660

Db	601	RRNCWSKTTCLHLATADAKAFPAHGDGQAFLTRIWWGDMAGTPIRLILGALFCLPALV	660
Qy	661	YTNLITFSEAPLRTGLDQLDLSLDTKESPLVGLQSRVEELVEAPRAQDGRGPRAVFL	720
Db	661	YTNLITFSEAPLRTGLDQLDLSLDTKESPLVGLQSRVEELVEAPRAQDGRGPRAVFL	720
Qy	721	LTRWRKFWGAPVTVFLGNVVMYFAFLFTVVLVDFRPPQPGSGPEVTLYFWVFTLVL	780
Db	721	LTRWRKFWGAPVTVFLGNVVMYFAFLFTVVLVDFRPPQPGSGPEVTLYFWVFTLVL	780
Qy	781	BEIRQGFPTDTHLVKKFTLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAFEAGRTVLAM	840
Db	781	BEIRQGFPTDTHLVKKFTLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAFEAGRTVLAM	840
Qy	841	DFWVFTLRLIHFALHKGQPKIIIVVERMKDVPFFLFLSVMLVAYGVTTQALLHPHDG	900
Db	841	DFWVFTLRLIHFALHKGQPKIIIVVERMKDVPFFLFLSVMLVAYGVTTQALLHPHDG	900
Qy	901	RLEWIFRVLRYRPIQIFGOIPLDEIDEARVNCSTHPLLEDSPCSPLYANWLIVILLV	960
Db	901	RLEWIFRVLRYRPIQIFGOIPLDEIDEARVNCSTHPLLEDSPCSPLYANWLIVILLV	960
Qy	961	TFLVNTVNLMLLIAMFSYTFQVVGNDMFWKFORYNLIIVEYHERPALAPPFILLSHL	1020
Db	961	TFLVNTVNLMLLIAMFSYTFQVVGNDMFWKFORYNLIIVEYHERPALAPPFILLSHL	1020
Qy	1021	SLTLRRVFKGAEHKKREHLERDLPDLPDQKVVTWETVQENFLSKWEKRRRDSGEVLRLK	1080
Db	1021	SLTLRRVFKGAEHKKREHLERDLPDLPDQKVVTWETVQENFLSKWEKRRRDSGEVLRLK	1080
Qy	1081	TAHRVDFITAKYLGGLREOEKRIKCLSQINYSVLVSSVADVLAQGGGPRSSOHCEGSGQ	1140
Db	1081	TAHRVDFITAKYLGGLREOEKRIKCLSQINYSVLVSSVADVLAQGGGPRSSOHCEGSGQ	1140
Qy	1141	LVAADHRGGLDGEQPGAGQPPSDT	1165
Db	1141	LVAADHRGGLDGEQPGAGQPPSDT	1165

RESULT 3

US-10-785-758-2

Sequence 2, Application US/10785758

Publication No. US20050019830A1

GENERAL INFORMATION:

APPLICANT: Penner, Reinhold

APPLICANT: Flieg, Andrea

TITLE OF INVENTION: Methods of Screening for TRPM5 Modulators

FILE REFERENCE: A-72155/RFT/THR (469324-00029)

CURRENT APPLICATION NUMBER: US/10/785,758

PRIOR FILING DATE: 2004-02-23

PRIOR APPLICATION NUMBER: US 60/448,955

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 1165

TYPE: PRT

ORGANISM: Homo sapiens

US-10-785-758-2

Query Match

Best Local Similarity 100.0%; Score 6093; DB 17; Length 1165;

Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MODVQGPSCGDAEDRELGLHRGEVNFVGGSGKKRKFVRVPSPGAPSVLPDILLAEW	60
Db	1	MODVQGPSCGDAEDRELGLHRGEVNFVGGSGKKRKFVRVPSPGAPSVLPDILLAEW	60
Qy	61	HLPAPLNVLVSGEEQPFAMKSWLRDLRLKGLVKAAQSTGAWILTSALRVLARHVGQAV	120
Db	61	HLPAPLNVLVSGEEQPFAMKSWLRDLRLKGLVKAAQSTGAWILTSALRVLARHVGQAV	120

RESULT 4

US-10-794-897-2
 ; Sequence 2, Application US/10794897
 ; Publication No. US20040259160A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnson, Jeffrey D.
 ; APPLICANT: Zhou, Yun-Ping
 ; APPLICANT: Metabolix, Inc.
 ; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
 ; FILE REFERENCE: 016325-019010US
 ; CURRENT APPLICATION NUMBER: US/10794,897
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: US 60/452,596
 ; PRIOR FILING DATE: 2003-03-05
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 1167
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human betaTRP (MTR1) calcium channel
 US-10-794-897-2

Query Match 99.8%; Score 6078; DB 16; Length 1167;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1164; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 QY 1 MQDVQGPFGSGDADRELGHRGEVNFPGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
 DB 1 MQDVQGPFGSGDADRELGHRGEVNFPGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
 QY 61 HLPAPNLVSLVGEQPFAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLARHVGQAV 120
 DB 61 HLPAPNLVSLVGEQPFAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLARHVGQAV 120
 QY 121 RDHSLASTSTKRVVAVGMASLGRVLRHRLLEAQAQ--EDFPVHYDEDDGGSGQPLCSLDS 178
 DB 121 RDHSLASTSTKRVVAVGMASLGRVLRHRLLEAQAQVHEDFPVHYDEDDGGSGQPLCSLDS 180
 QY 179 NLSHFVLVPGPGKDGGLTELRLEKHISORAGYGGTSGIEIPVLCILVNGDPNTLE 238
 DB 181 NLSHFVLVPGPGKDGGLTELRLEKHISORAGYGGTSGIEIPVLCILVNGDPNTLE 240
 QY 239 RISRAVEQAAPWLLVVGSGGIADVLAAVLPVQPHLLVPKVAEKQKFPKSFHFWEDIVR 298
 DB 241 RISRAVEQAAPWLLVVGSGGIADVLAAVLPVQPHLLVPKVAEKQKFPKSFHFWEDIVR 300
 QY 299 WTKLLQNTITSHOHLTVYDFQEGSEELDTVLKALVKAACKSHSQBPQDYLDLKLAVAW 358
 DB 301 WTKLLQNTITSHOHLTVYDFQEGSEELDTVLKALVKAACKSHSQBPQDYLDLKLAVAW 360
 QY 359 DRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOEL 418
 DB 361 DRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOEL 420
 QY 419 YRSVSRKSLLDLQKQSEARLTLAGLGTQQAQREPAPPPAPSLHVSRLVKDLQDAC 478
 DB 421 YRSVSRKSLLDLQKQSEARLTLAGLGTQQAQREPAPPPAPSLHVSRLVKDLQDAC 480
 QY 479 RGFYQDGRPGDRRAEKGPAKRPQTQKWLDDLNKSENPRDLFLMAVLQNRHEMATYFW 538
 DB 481 RGFYQDGRPGDRRAEKGPAKRPQTQKWLDDLNKSENPRDLFLMAVLQNRHEMATYFW 540
 QY 539 AMGEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECVSNSEARAFAL 598
 DB 541 AMGEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECVSNSEARAFAL 600
 QY 599 LVRRNRCSWTKTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAACTPIILRLGAPLCPA 658
 DB 601 LVRRNRCSWTKTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAACTPIILRLGAPLCPA 660

QY 659 LVYTNLITFSBEAPLRTGLIEDLQDLSLDTSEKSPLYGLQSRVEELVAPRAQGRGPRAV 718
 DB 661 LVYTNLITFSBEAPLRTGLIEDLQDLSLDTSEKSPLYGLQSRVEELVAPRAQGRGPRAV 720
 QY 719 FLLTRWRKFWGAPVTVFLGNVMYFAFLFTYVLLVDFRPPPGPGSGPEVTLYFWVFTL 778
 DB 721 FLLTRWRKFWGAPVTVFLGNVMYFAFLFTYVLLVDFRPPPGPGSGPEVTLYFWVFTL 780
 QY 779 VLEETROGFFDDETHLVKFFTLVGNWNKCDMVAIFLFIIVGVTCTMLPSAFEAGRTVL 838
 DB 781 VLEETROGFFDDETHLVKFFTLVGNWNKCDMVAIFLFIIVGVTCTMLPSAFEAGRTVL 840
 QY 839 AMDFMVFTLRILHIFAIHKOLGPKIIIVERMKDVFPLFELFSLVWLVAYGVTTQALLHPH 898
 DB 841 AMDFMVFTLRILHIFAIHKOLGPKIIIVERMKDVFPLFELFSLVWLVAYGVTTQALLHPH 900
 QY 899 DGRLEWIFRRVLYPYLQIFQIPDLDEIDARVNCSTHPLLEDSPSCSLYANMLVILL 958
 DB 901 DGRLEWIFRRVLYPYLQIFQIPDLDEIDARVNCSTHPLLEDSPSCSLYANMLVILL 960
 QY 959 LVTFLLVTVNLLMNLIIAMFSYTFVQVGNADMFQKFORNLIVEYHERPALAPPFILLS 1018
 DB 961 LVTFLLVTVNLLMNLIIAMFSYTFVQVGNADMFQKFORNLIVEYHERPALAPPFILLS 1020
 QY 1019 HLSITLRVFPKBAEHKREHLERDLPDLDQKVVTWETQKENFLSKMEKRRRDSGEVL 1078
 DB 1021 HLSITLRVFPKBAEHKREHLERDLPDLDQKVVTWETQKENFLSKMEKRRRDSGEVL 1080
 QY 1079 RKTARHVDFTAKYLGRLRQEKRIKLESQINCSVLVSSVADVLAAQGGPRSSQHCGBG 1138
 DB 1081 RKTARHVDFTAKYLGRLRQEKRIKLESQINCSVLVSSVADVLAAQGGPRSSQHCGBG 1140
 QY 1139 SOLVAADHRGGLDGEWQPGAGPPSDT 1165
 DB 1141 SOLVAADHRGGLDGEWQPGAGPPSDT 1167

RESULT 5
 US-09-834-792-5
 ; Sequence 5, Application US/09834792
 ; Patent No. US20020037515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mount Sinai School of Medicine of NYU
 ; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
 ; TITLE OF INVENTION: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
 ; FILE REFERENCE: AP32911 070165.0589
 ; CURRENT APPLICATION NUMBER: US/09/834,792
 ; CURRENT FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/197,491
 ; PRIOR FILING DATE: 2000-04-17
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1164
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-834-792-5
 Query Match 99.4%; Score 6057.5; DB 9; Length 1164;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1161; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
 QY 1 MQDVQGPFGSGDADRELGHRGEVNFPGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
 DB 1 MQDVQGPFGSGDADRELGHRGEVNFPGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
 QY 61 HLPAPNLVSLVGEQPFAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLARHVGQAV 120
 DB 61 HLPAPNLVSLVGEQPFAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLARHVGQAV 120
 QY 121 RDHSLASTSTKRVVAVGMASLGRVLRHRLLEAQAQ--EDFPVHYDEDDGGSGQPLCSLDS 180
 DB 121 RDHSLASTSTKRVVAVGMASLGRVLRHRLLEAQAQ--EDFPVHYDEDDGGSGQPLCSLDS 180

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181 SHFVLVEPGPGKGDGLTELRLRLEKHI SEORAGYGGTSGSIEIPVLCLLVNGDPTLRI 240
181 SHFVLVEPGPGKGDGLTELRLRLEKHI SEORAGYGGTSGSIEIPVLCLLVNGDPTLRI 240
241 SRVVEQAAPWLLVVGSGGIADVLAALVNQPHLLVPKVAEKQKFKFSPKSHFSEWEDIVRWT 300
241 SRVVEQAAPWLLVVGSGGIADVLAALVNQPHLLVPKVAEKQKFKFSPKSHFSEWEDIVRWT 300
301 KLLQNTITSHOHLITVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDELKLA VAWDR 360
301 KLLQNTITSHOHLITVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDELKLA VAWDR 360
361 VDIKSEIFNGDVVEKSCDLEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOEYL 420
361 VDIKSEIFNGDVVEKSCDLEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOEYL 420
421 SVSRKSLLDLLQKQEEARLTLAGLGTQQAEPAPGPPAFSLHEVSRVLKDFLODACRG 480
421 SVSRKSLLDLLQKQEEARLTLAGLGTQQAEPAPGPPAFSLHEVSRVLKDFLODACRG 480
481 FYQDGRPGDRRRAEKGPAKPTGQKWLDDLNOKSENPRDLFLMVLQNRHEMATYFWAM 540
481 FYQDGRPGDRRRAEKGPAKPTGQKWLDDLNOKSENPRDLFLMVLQNRHEMATYFWAM 540
541 GOEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARFALLV 600
541 GOEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARFALLV 600
601 RNRNCWSKTTCLHLATEADAKAFPAHDGVQAFELTRIWMGDMAGTPIILLLGAFCLPALV 660
601 RNRNCWSKTTCLHLATEADAKAFPAHDGVQAFELTRIWMGDMAGTPIILLLGAFCLPALV 660
661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAGDRGPRAVFL 720
661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAGDRGPRAVFL 720
721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQPGSPGPEVTLFWFVFTVL 780
721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQPGSPGPEVTLFWFVFTVL 780
781 EIRQGFETDEDTHLVKKTFLYVGDNNKCDMVAIFLFIWGTCTMLPSAFAGRTVLAM 840
781 EIRQGFETDEDTHLVKKTFLYVGDNNKCDMVAIFLFIWGTCTMLPSAFAGRTVLAM 840
841 DFVWFTLRILHIFAIHKQGPKIIVVERMMKDVFFFLFVSVMLVAYGVTTQALLHPHDG 900
841 DFVWFTLRILHIFAIHKQGPKIIVVERMMKDVFFFLFVSVMLVAYGVTTQALLHPHDG 900
901 RLEWIFRRVLYRPLYQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
901 RLEWIFRRVLYRPLYQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
961 TELLVNTNLLMNLIIAMFSTFOVQGNADMFWKFORYNLI VEYHERPALAPPFILLSHL 1020
961 TELLVNTNLLMNLIIAMFSTFOVQGNADMFWKFORYNLI VEYHERPALAPPFILLSHL 1020
1021 SLTLRRVFKKEAHEKREHLERDLPDLDQKVVTWETVQKENFLSKMEKRRRDSGEVLARK 1080
1021 SLTLRRVFKKEAHEKREHLERDLPDLDQKVVTWETVQKENFLSKMEKRRRDSGEVLARK 1080
1081 TAHRVDFIAKYLGLREQKRIKCLSEQINYCSVLVSSVADVLAAQGGPRSSOHCCEGSG 1140
1081 TAHRVDFIAKYLGLREQKRIKCLSEQINYCSVLVSSVADVLAAQGGPRSSOHCCEGSG 1140
1141 LVAADHGGIDGWEOPCAGOPPST 1165
1141 LVAADHGGIDGWEOPCAGOPPST 1165

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RESULT 6
US-10-794-897-7
; Sequence 7, Application US/10794897

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; Publication No. US20040259160A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Zhou, Yun-Ping
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes and Related Diseases Involving Beta-TRP
; FILE REFERENCE: 016325-019010US
; CURRENT APPLICATION NUMBER: US/10794.897
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/452,596
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human betaTRP (MBX) calcium channel
US-10-794-897-7

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Query Match 98.2%; Score 5985; DB 16; Length 1165;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 1 MDVQGPSPGPGDAEDRRRLGLHRGEVNFVGGSGKRGKFKVVRPSGVAPSVLFDLLAEW 60
DB 1 MDVQGPSPGPGDAEDRRRLGLHRGEVNFVGGSGKRGKFKVVRPSGVAPSVLFDLLAEW 60
QY 61 HLPANLVVSLVGEQPPFAMKSWLDRVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
DB 61 HLPANLVVSLVGEQPPFAMKSWLDRVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
QY 121 RDHSLASTSTKRVVAVGMAISLCRVLHRIIEEAQEDFPVHYPEDDGSGQGLCSLDSNL 180
DB 121 RDHSLASTSTKRVVAVGMAISLCRVLHRIIEEAQEDFPVHYPEDDGSGQGLCSLDSNL 180
QY 181 SHFVLVEPGPGKGDGLTELRLRLEKHI SEORAGYGGTSGSIEIPVLCLLVNGDPTLRI 240
DB 181 SHFVLVEPGPGKGDGLTELRLRLEKHI SEORAGYGGTSGSIEIPVLCLLVNGDPTLRI 240
QY 241 SRVVEQAAPWLLVVGSGGIADVLAALVNQPHLLVPKVAEKQKFKFSPKSHFSEWEDIVRWT 300
DB 241 SRVVEQAAPWLLVVGSGGIADVLAALVNQPHLLVPKVAEKQKFKFSPKSHFSEWEDIVRWT 300
QY 301 KLLQNTITSHOHLITVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDELKLA VAWDR 360
DB 301 KLLQNTITSHOHLITVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDELKLA VAWDR 360
QY 361 VDIKSEIFNGDVVEKSCDLEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOEYL 420
DB 361 VDIKSEIFNGDVVEKSCDLEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOEYL 420
QY 421 SVSRKSLLDLLQKQEEARLTLAGLGTQQAEPAPGPPAFSLHEVSRVLKDFLODACRG 480
DB 421 SVSRKSLLDLLQKQEEARLTLAGLGTQQAEPAPGPPAFSLHEVSRVLKDFLODACRG 480
QY 481 FYQDGRPGDRRRAEKGPAKPTGQKWLDDLNOKSENPRDLFLMVLQNRHEMATYFWAM 540
DB 481 FYQDGRPGDRRRAEKGPAKPTGQKWLDDLNOKSENPRDLFLMVLQNRHEMATYFWAM 540
QY 541 GOEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARFALLV 600
DB 541 GOEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARFALLV 600
QY 601 RNRNCWSKTTCLHLATEADAKAFPAHDGVQAFELTRIWMGDMAGTPIILLLGAFCLPALV 660
DB 601 RNRNCWSKTTCLHLATEADAKAFPAHDGVQAFELTRIWMGDMAGTPIILLLGAFCLPALV 660
QY 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAGDRGPRAVFL 720
DB 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAGDRGPRAVFL 720

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US-10-794-897-8

Query Match 84.3%; Score 5134.5; DB 16; Length 1168;
Best Local Similarity 84.8%; Pred. No. 0;
Matches 990; Conservative 61; Mismatches 114; Indels 3; Gaps 2;

Qy 1 MODVGPDPGDAEDRRLGLHGEVNFVGGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
Db 1 MOXVSSCPGPPDTEGWEPLCRGEVNFVGGSGKRGKRVFVPSGVAPSVLFDLLAEW 60

Qy 61 HLPAPNLVSVLGEERPFAMKSWLRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120
Db 61 HLPAPNLVSVLGEERPFAMKSWLRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120

Qy 121 RDHSLASTSKRVVAVGASLGRVILHRRILEAQ--EDFPVHYPEDDGGSGPLCSLDS 178
Db 121 RDHSLASTSKRVVAVGASLGRVILHRRILEAQ--EDFPVHYPEDDGGSGPLCSLDS 180

Qy 179 NLSHFILVEPGVGLSGNDGLTELQSLKHISQQRGTGVTSSIQIPVLCVLLVNGDPNTL 237
Db 181 NLSHFILVEPGVGLSGNDGLTELQSLKHISQQRGTGVTSSIQIPVLCVLLVNGDPNTL 240

Qy 238 ERISRAVEQAAPWLILVSGGGIADVLAAVNOPHLLVPKVAEKQPKFPPSKHFSWEDIV 297
Db 241 ERISRAVEQAAPWLILVSGGGIADVLAAVNOPHLLVPKVAEKQPREKPPSCFSEWAI 300

Qy 298 RWTKLLQNTSHOHLITVDFPEQSGEELDTVILKALVKAKSHSQEPQDYLDLKLAVA 357
Db 301 HMTPELLQNTIAHPHLLTVDFPEQSGEELDTVILKALVKAKSHSQEADYLDLKLAVA 360

Qy 358 WDRVDIAKSEIENGVEWKSCLDEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 417
Db 361 WDRVDIAKSEIENGVEWKSCLDEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 420

Qy 418 LYRSVSRKSLLPOLLQKOEARELTLAGLQTOQAREPPAGPAPFSLHVSRLKDFLODA 477
Db 421 LYHSVSPKSLLPOLLQKOEARELTLAGLQTOQAREPPAGPAPFSLHVSRLKDFLODA 480

Qy 478 CRGFYODGRPDRRAEKGPAPKPTQCKWLLDLNOKSENPDWDLFLWAVLQNRHEMATYF 537
Db 481 CRGFYODGRPDRRAEKGPAPKPTQCKWLLDLNOKSENPDWDLFLWAVLQNRHEMATYF 540

Qy 538 WAMQEGVAAALAAKILKEMSHLEAEAAATREAKYERLALDLFSECYNSERAPFA 597
Db 541 WAMQEGVAAALAAKILKEMSHLEAEAVRTMREAKYERLALDLFSECYNSERAPFA 600

Qy 598 LLVRRNCWKTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAGTPIRLLLGAFLCP 657
Db 601 LLVRRNCWKTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAGTPIRLLLGAFLCP 660

Qy 658 ALVYTNLITFSEAPLRTGLELDLQDLSLQTEKSPLYGLQSRVEELVEAPRAQDGRPA 717
Db 661 ALVYTNLITFSEAPLRTGLELDLQDLSLQTEKSPLYGLQSRVEELVEAPRAQDGRPA 720

Qy 718 VELLITWRKFWGAPVTVFLGNVVMYFAPLFTYVLLVDFRPPQPGSGEVTLTYFWVFT 777
Db 721 AFLLITWRKFWGAPVTVFLGNVVMYFAPLFTYVLLVDFRPPQPGSGEVTLTYFWVFT 780

Qy 778 LVLEERIQGFPTDEDTHLVKKFTLYVGDNWNKCDMVAIFLIVGVTCRMLPSAFEAGRTV 837
Db 781 LVLEERIQGFPTDEDTHLVKKFTLYVGDNWNKCDMVAIFLIVGVTCRMLPSAFEAGRTV 840

Qy 838 LAMDFWFTLRLIHI FAHKQLGPKIIVVERMKDVPFFLFFLSVMLVAYGVTTQALLHP 897
Db 841 LAMDFWFTLRLIHI FAHKQLGPKIIVVERMKDVPFFLFFLSVMLVAYGVTTQALLHP 900

Qy 898 HDGRLEWIFRVLRYPLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCSLVANMLVIL 957
Db 901 HDGRLEWIFRVLRYPLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCSLVANMLVIL 960

Qy 958 LLVTFLLVTVNLLMNLIAFSTFQVQGNADMFVKFQRYNLIYEHERPALAPPFILL 1017
Db 961 LLVTFLLVTVNLLMNLIAFSTFQVQGNADMFVKFQRYNLIYEHERPALAPPFILL 1020

US-09-834-792-2

Query Match 83.5%; Score 5088.5; DB 9; Length 1158;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

Qy 1 MODVGPDPGDAEDRRLGLHGEVNFVGGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
Db 1 MOTTOSCPGPPDTEGWEPLCRGEVNFVGGSGKRGKRVFVPSGVAPSVLFDLLAEW 60

Qy 61 HLPAPNLVSVLGEERPFAMKSWLRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120
Db 61 HLPAPNLVSVLGEERPFAMKSWLRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120

Qy 121 RDHSLASTSKRVVAVGASLGRVILHRRILEAQ--EDFPVHYPEDDGGSGPLCSLDS 178
Db 121 RDHSLASTSKRVVAVGASLGRVILHRRILEAQ--EDFPVHYPEDDGGSGPLCSLDS 180

Qy 179 NLSHFILVEPGVGLSGNDGLTELQSLKHISQQRGTGVTSSIQIPVLCVLLVNGDPNTL 237
Db 181 NLSHFILVEPGVGLSGNDGLTELQSLKHISQQRGTGVTSSIQIPVLCVLLVNGDPNTL 240

Qy 238 ERISRAVEQAAPWLILVSGGGIADVLAAVNOPHLLVPKVAEKQPKFPPSKHFSWEDIV 297
Db 241 ERISRAVEQAAPWLILVSGGGIADVLAAVNOPHLLVPKVAEKQPREKPPSCFSEWAI 300

Qy 298 RWTKLLQNTSHOHLITVDFPEQSGEELDTVILKALVKAKSHSQEPQDYLDLKLAVA 357
Db 301 HMTPELLQNTIAHPHLLTVDFPEQSGEELDTVILKALVKAKSHSQEADYLDLKLAVA 360

Qy 358 WDRVDIAKSEIENGVEWKSCLDEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 417
Db 361 WDRVDIAKSEIENGVEWKSCLDEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 420

Qy 418 LYRSVSRKSLLPOLLQKOEARELTLAGLQTOQAREPPAGPAPFSLHVSRLKDFLODA 477
Db 421 LYHSVSPKSLLPOLLQKOEARELTLAGLQTOQAREPPAGPAPFSLHVSRLKDFLODA 480

Qy 478 CRGFYODGRPDRRAEKGPAPKPTQCKWLLDLNOKSENPDWDLFLWAVLQNRHEMATYF 537
Db 481 CRGFYODGRPDRRAEKGPAPKPTQCKWLLDLNOKSENPDWDLFLWAVLQNRHEMATYF 540

Qy 538 WAMQEGVAAALAAKILKEMSHLEAEAAATREAKYERLALDLFSECYNSERAPFA 597
Db 541 WAMQEGVAAALAAKILKEMSHLEAEAVRTMREAKYERLALDLFSECYNSERAPFA 600

Qy 598 LLVRRNCWKTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAGTPIRLLLGAFLCP 657
Db 601 LLVRRNCWKTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAGTPIRLLLGAFLCP 660

Qy 658 ALVYTNLITFSEAPLRTGLELDLQDLSLQTEKSPLYGLQSRVEELVEAPRAQDGRPA 717
Db 661 ALVYTNLITFSEAPLRTGLELDLQDLSLQTEKSPLYGLQSRVEELVEAPRAQDGRPA 720

Qy 718 VELLITWRKFWGAPVTVFLGNVVMYFAPLFTYVLLVDFRPPQPGSGEVTLTYFWVFT 777
Db 721 AFLLITWRKFWGAPVTVFLGNVVMYFAPLFTYVLLVDFRPPQPGSGEVTLTYFWVFT 780

Qy 778 LVLEERIQGFPTDEDTHLVKKFTLYVGDNWNKCDMVAIFLIVGVTCRMLPSAFEAGRTV 837
Db 781 LVLEERIQGFPTDEDTHLVKKFTLYVGDNWNKCDMVAIFLIVGVTCRMLPSAFEAGRTV 840

Qy 838 LAMDFWFTLRLIHI FAHKQLGPKIIVVERMKDVPFFLFFLSVMLVAYGVTTQALLHP 897
Db 841 LAMDFWFTLRLIHI FAHKQLGPKIIVVERMKDVPFFLFFLSVMLVAYGVTTQALLHP 900

Qy 898 HDGRLEWIFRVLRYPLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCSLVANMLVIL 957
Db 901 HDGRLEWIFRVLRYPLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCSLVANMLVIL 960

Qy 958 LLVTFLLVTVNLLMNLIAFSTFQVQGNADMFVKFQRYNLIYEHERPALAPPFILL 1017
Db 961 LLVTFLLVTVNLLMNLIAFSTFQVQGNADMFVKFQRYNLIYEHERPALAPPFILL 1020

Db 481 CRGYQDG-----RRMEERGPKPKACQKWLPLSRKSDPWRDLFLMAVLQNRVEMATYF 536
 Qy 538 WAMQGEVAAALAAACKILKEMSHLETEAEAAATREAKYERIALDLFSECVSNSEARAF 597
 Db 537 WAMRGVAAALAAACKIIKEMSHLEKEAEAVARTREAKYEQALDLFSECVSNSEARAF 596
 Qy 598 LLVRRNRCSKTTCLHLATEADAKAFFAHGQVQAFITRIWGDMAAGTPIRLILGALCP 657
 Db 597 LLVRRNHSRITCLHLATEADAKAFFAHGQVQAFITRIWGDMAAGTPIRLILGALCP 656
 Qy 658 ALVYTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVBEVLEAPRAQDGRPA 717
 Db 657 ALIYTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVBEVLEAPRAQDGRPA 716
 Qy 718 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFTVYLLVDRPPPPQSGSEVTLVFWVFT 777
 Db 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTVYLLVDRPPPPQSGSEVTLVFWVFT 776
 Qy 778 LVLEIRQGFTEDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTV 837
 Db 777 LVLEIRQGFTEDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTV 836
 Qy 838 LAMDPMVFTLRIHFAHKLQGPKIIVVERMMKQVFFFLFSLVNLVAYGVTTQALLHP 897
 Db 837 LAIDPMVFTLRIHFAHKLQGPKIIVVERMMKQVFFFLFSLVNLVAYGVTTQALLHP 896
 Qy 898 HDGRLEWIFRVLRYPLQIPGQIPDLDEIDEARVNCSTHPLLEDSPSCPSLYANLVL 957
 Db 897 HDGRLEWIFRVLRYPLQIPGQIPDLDEIDEARVNCSTHPLLEDSPSCPSLYANLVL 956
 Qy 958 LLVTFLLVNTVLLNLLIAMFSYTFVQVGNADMFVKFORNLIYVHERPALAPFFILL 1017
 Db 957 LLVTFLLVNTVLLNLLIAMFSYTFVQVGNADMFVKFORNLIYVHERPALAPFFILL 1016
 Qy 1018 SHLSLTLRRVFKAEHKEHLERDLPDQKVVTWETVQKENFLSKMEKRRDSEGEV 1077
 Db 1017 SHLSLTLRRVFKAEHKEHLERDLPDQKVVTWETVQKENFLSKMEKRRDSEGEV 1076
 Qy 1078 LRKTAHRVDRIAKYGLGRQEKRIKLESQINYSVLVSVADVLAQGGPRSSHQGE 1137
 Db 1077 LRKTAHRVDRIAKYGLGRQEKRIKLESQINYSVLVSVADVLAQGGPRSSHQGE 1136
 Qy 1138 GSQVLAADHGGDQWEGQAGQPPSDT 1165
 Db 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 9

; US-10-026-188-5
 ; Sequence 5, Application US/10026188
 ; Publication No. US20020164645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Zhang, Yifeng
 ; TITLE OF INVENTION: The Regents of the University of California
 ; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
 ; TITLE OF INVENTION: Ion Channel
 ; FILE REFERENCE: 02307E-114910US
 ; CURRENT APPLICATION NUMBER: US/10/026.188
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 1158
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; OTHER INFORMATION: mouse ltrpc5 predicted amino acid sequence
 ; US-10-026-188-5

Query Match

83.5%; Score 5088.5; DB 13; Length 1158;

Best Local Similarity 84.1%; Pred. No. 0;

Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

Qy 1 MODVQPPRPGSDAEDRRRLGLHRGEVNFSGSKGKGVVRVPSGVAPSVLPDLLAEW 60
 Db 1 MQTQSSCPGPPDTEDEWEPILCRGEINFGSGKGGKGVVRVPSGVAPSVLPDLLAEW 60
 Qy 61 HLPAPNLVSVLVBGEPPFAMKSWLRDLVRKGLKAAQSTGAWILTSALRVGLARHVQAV 120
 Db 61 HLPAPNLVSVLVBGEPPFAMKSWLRDLVRKGLKAAQSTGAWILTSALRVGLARHVQAV 120
 Qy 121 RDHSLASTSTKRVVAVVAVMASLGRVLRHLE--EAQEDPPVHYPPDDGSGQSPCLSDS 178
 Db 121 RDHSLASTSTKRVVAVVAVMASLGRVLRHLE--EAQEDPPVHYPPDDGSGQSPCLSDS 178
 Qy 179 NLSHIFILVEPPPPGKG-DGITELRLEKHSISQRAGYGGTGTGIEPIVLCVLVNGDPNTL 237
 Db 181 NLSHIFILVESGALSGNDGLTELQSLKHSISQRTGYGGTGTGIEPIVLCVLVNGDPNTL 240
 Qy 238 ERISRAVEQAAPMLILVSGGIADVLAAVNOHPLLVPKVAEKQPKPKPSKHFSWEDIV 297
 Db 241 ERISRAVEQAAPMLILVSGGIADVLAAVNOHPLLVPKVAEKQPKPKPSKHFSWEDIV 297
 Qy 298 RWTKLQNTSHOHLITVYDFEQEGSEELDTVLKALVKACKSHSQEADQYLDLKLAVA 357
 Db 301 HWTLLQNTIAAHPHLLITVYDFEQEGSEELDTVLKALVKACKSHSQEADQYLDLKLAVA 360
 Qy 358 WDRVDIAKSIIFNGDVWEMKSCDLEEVMDALVSNKPEFVRLVFNAGDVAADPLTYGRLO 417
 Db 361 WDRVDIAKSIIFNGDVWEMKSCDLEEVMDALVSNKPEFVRLVFNAGDVAADPLTYGRLO 420
 Qy 418 LYSVGRKSLFDLQKQKEBARLTLAGLGTQQAEPPEAGPPAPSLHVSRLVDKLODA 477
 Db 421 LYSVGRKSLFDLQKQKEBARLTLAGLGTQQAEPPEAGPPAPSLHVSRLVDKLODA 480
 Qy 478 CRGYQDGPRGRRRAEAKGPAKPTGQKWLDLNOKSNPWRDLFLMAVLQNRHEMATYF 537
 Db 481 CRGYQDGPRGRRRAEAKGPAKPTGQKWLDLNOKSNPWRDLFLMAVLQNRHEMATYF 536
 Qy 538 WAMQGEVAAALAAACKILKEMSHLETEAEAAATREAKYERIALDLFSECVSNSEARAF 597
 Db 537 WAMQGEVAAALAAACKILKEMSHLETEAEAAATREAKYERIALDLFSECVSNSEARAF 596
 Qy 598 LLVRRNRCSKTTCLHLATEADAKAFFAHGQVQAFITRIWGDMAAGTPIRLILGALCP 657
 Db 597 LLVRRNRCSKTTCLHLATEADAKAFFAHGQVQAFITRIWGDMAAGTPIRLILGALCP 656
 Qy 658 ALVYTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVBEVLEAPRAQDGRPA 717
 Db 657 ALIYTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVBEVLEAPRAQDGRPA 716
 Qy 718 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFTVYLLVDRPPPPQSGSEVTLVFWVFT 777
 Db 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTVYLLVDRPPPPQSGSEVTLVFWVFT 776
 Qy 778 LVLEIRQGFTEDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTV 837
 Db 777 LVLEIRQGFTEDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTV 836
 Qy 838 LAMDPMVFTLRIHFAHKLQGPKIIVVERMMKQVFFFLFSLVNLVAYGVTTQALLHP 897
 Db 837 LAIDPMVFTLRIHFAHKLQGPKIIVVERMMKQVFFFLFSLVNLVAYGVTTQALLHP 896
 Qy 898 HDGRLEWIFRVLRYPLQIPGQIPDLDEIDEARVNCSTHPLLEDSPSCPSLYANLVL 957
 Db 897 HDGRLEWIFRVLRYPLQIPGQIPDLDEIDEARVNCSTHPLLEDSPSCPSLYANLVL 956
 Qy 958 LLVTFLLVNTVLLNLLIAMFSYTFVQVGNADMFVKFORNLIYVHERPALAPFFILL 1017
 Db 957 LLVTFLLVNTVLLNLLIAMFSYTFVQVGNADMFVKFORNLIYVHERPALAPFFILL 1016
 Qy 1018 SHLSLTLRRVFKAEHKEHLERDLPDQKVVTWETVQKENFLSKMEKRRDSEGEV 1077

Db 1017 SHLSLVKQVFRKEAQRKQHLERDLPDLPDQKIITWETQKCNFLSTMKRRRSEGEV 1076
Qy 1078 LRKTAHRVDFTAKYLGGLREGEKRIKLESQINVCVSVLVSSVADVLAQGGGPRSSQHCGE 1137
Db 1077 LRKTAHRVDLITAKYIGGLREGEKRIKLESQANQYCMILLSSMTDTLPGGYTSSQNCGC 1136
Qy 1138 GSQLVAADHRGGLDGEQPGAGQPPSDT 1165
Db 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 10
US-10-794-897-4
; Sequence 4, Application US/10794897
; Publication NO. US20040259160A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Zhou, Yun-Ping
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes and Related Diseases Involving Beta-TRP
; FILE REFERENCE: 016325-019010US
; CURRENT APPLICATION NUMBER: US/10/794,897
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/452,596
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse betaTRP (TRPM5) calcium channel
US-10-794-897-4

Query Match 83.5%; Score 5088.5; DB 16; Length 1158;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

Qy 1 MDVQGPSPGDAEDRELGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFDLLAPW 60
Db 1 MQTQSSCGSPDTEGWEPILCRGEINFGSGKRGKFRVPSGVAPSVLFDLLTEW 60
Qy 61 HLPAPNLVSLVGEOPFAMKWLRLVLRKGLVKAQSTGAMILTSALVGLARHVQAV 120
Db 61 HLPAPNLVSLVGEERPLAMKWLRLVLRKGLVKAQSTGAMILTSALVGLARHVQAV 120
Qy 121 RDSLASTSTKVRVAVGASLGRVLRHRLILE--EAQEDFPVHYREDGSGSQPLCSLDS 178
Db 121 RDSLASTSTKIRVVAIGASLDRILHRLQLLDGVHOKEDTPPIHYPADEGNIQGPLCLDS 180
Qy 179 NLSHFTLVPPGPKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPVLCILVNGDPNTL 237
Db 181 NLSHFTLVPSGALSGNDGLTELQSLKHXISQRTGYGTSCTQIPVLCILVNGDPNTL 240
Qy 238 ERISRAVEQAAPMLIIVGSGGIADVLAAALVNPHLLVPKVAEKQFKPEKPPSHFSEWIV 297
Db 241 ERISRAVEQAAPMLIIVGSGGIADVLAAALVNPHLLVPKVAEKQFKPEKPPSECFSEWIV 300
Qy 298 RWTKLQNTSHOHLITVYDFEAGESELDVTILKALVKACKSHSOEPDYLDELKLA 357
Db 301 HWTELLQNTAAHPHLLITVYDFEAGESELDVTILKALVKACKSHSOEAQDYLDELKLA 360
Qy 358 WDRVDIAKSIIFNGDVEMKSCDLEEVNVDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 417
Db 361 WDRVDIAKSIIFNGDVEMKSCDLEEVNMTDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 420
Qy 418 LYRSVSRKSLFLDLQKQBEARLTLAGTQOARBPAPGAPFAPSLHEVSRVLKDFLQDA 477
Db 421 LYHSVSPKSLFELLQKKEEGLTLAGLGAQQAARELPFGLPAPFAPSLHEVSRVLKDFLQDA 480
Qy 478 CRGFYQDGRGDRRAEKGPAKPTGQKWLIDLNQSENPRDLFLWAVLQNRHEMATYF 537

Db 481 CRGFYQDGRGDRRAEKGPAKPTGQKWLIDLNQSENPRDLFLWAVLQNRHEMATYF 536
Qy 538 WAMQEGVAAALAAACKILKEMSHLETEAARAPREAKYERLALDLFSECYSNSEARAF 597
Db 537 WAMQEGVAAALAAACKILKEMSHLEKEAEVARTWEAKYEQALDLFSECYGNSEADRA 596
Qy 598 LLVRNRCWSKTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPIRLILGAFCLP 657
Db 597 LLVRNHSWRTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPIRLILGAFCLP 656
Qy 717 ALVVTNLTSEAPLRTGLDQLDSDTEKSPLYGQSRVEELVEAPRAQDGRGPA 717
Db 657 ALIYTNLTSEAPLRTGLDQLDSDTEKSPLYGQSRVEELVEAPRAQDGRGPA 716
Qy 718 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPGSGSPVTVLYFWYFT 777
Db 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPGSGSPVTVLYFWYFT 776
Qy 778 LVLEBIRQGFPTDTHLVKKFTLYVGNMNMKDMVAIFLFIIVGVTCTMLPSAFAEAGRTV 837
Db 777 LVLEBIRQGFPTDTHLVKKFTLYVGNMNMKDMVAIFLFIIVGVTCTMLPSAFAEAGRTV 836
Qy 838 LAMDPMVFTLRIHFAHKQLGPKLIIVBERMKDVFPEFLFSLVWLVAVGVTTOALLHP 897
Db 837 LAIDPMVFTLRIHFAHKQLGPKLIIVBERMKDVFPEFLFSLVWLVAVGVTTOALLHP 896
Qy 898 HDGRLEWIFRFRVLRPYLQIFGOIPDLDEIDARVNCSTHPLLEDSPSCPSLYANLWVL 957
Db 897 HDGRLEWIFRFRVLRPYLQIFGOIPDLDEIDARVNCSTHPLLEDSPSCPSLYANLWVL 956
Qy 958 LLVTFLLVTNVLNMLLIAMFSTYTFQVVGQNMDFKQRYNLIIVEYHERPALAPPFILL 1017
Db 957 LLVTFLLVTNVLNMLLIAMFSTYTFQVVGQNMDFKQRYNLIIVEYHERPALAPPFILL 1016
Qy 1018 SHLSJTLRVRFKKAEHGREHLERDLPDLPDQKIITWETQKCNFLSTMKRRRSEGEV 1077
Db 1017 SHLSJTLRVRFKKAEHGREHLERDLPDLPDQKIITWETQKCNFLSTMKRRRSEGEV 1076
Qy 1078 LRKTAHRVDFTAKYLGGLREGEKRIKLESQINVCVSVLVSSVADVLAQGGGPRSSQHCGE 1137
Db 1077 LRKTAHRVDLITAKYIGGLREGEKRIKLESQANQYCMILLSSMTDTLPGGYTSSQNCGC 1136
Qy 1138 GSQLVAADHRGGLDGEQPGAGQPPSDT 1165
Db 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 11
US-10-794-897-6
; Sequence 6, Application US/10794897
; Publication NO. US20040259160A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Zhou, Yun-Ping
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes and Related Diseases Involving Beta-TRP
; FILE REFERENCE: 016325-019010US
; CURRENT APPLICATION NUMBER: US/10/794,897
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/452,596
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1156
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat betaTRP calcium channel
US-10-794-897-6


```
Query Match      82.5%; Score 5025.5; DB 16; Length 1156;
Best Local Similarity 83.0%; Pred. No. 0;
Matches 968; Conservative 75; Mismatches 112; Indels 11; Gaps 3;

QY 1 MDVQGPDPGSGDAEDRRLGLHGEVNFVGGSGKRGKRVPSGVAPSVLFDLLLAEW 60
Db 1 MPMAQSSCPGSPDPTDGDWEVLCKEGVNFVGGSGKSKFVKVPSNVAPSMLELLLTW 60
QY 61 HLPAPNLVSVLGEVQPFAMKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGOAV 120
Db 61 HLPAPNLVSVLGEERLFAKMSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGOAV 120
QY 121 RDHSLASTSTKVRVAVGMSASGLRVLRHRLLEAEQEDFPVHYPEDDGGSGPLCSLDSNL 180
Db 121 RDHSLASTSTKVRVAVGMSASGLRVLRHRLLEAEQEDFPVHYPEDDGGSGPLCSLDSNL 180
QY 181 SHFILVPEPTLGSNDGLAEQLSLEKHSQRTGYGTSIQIPVLCLLVNGDPSTLER 239
Db 181 SHFILVPEPTLGSNDGLAEQLSLEKHSQRTGYGTSIQIPVLCLLVNGDPSTLER 240
QY 240 ISRAVEQAAPWLILVSGGDIADVLAAALVNQPHLLVPKVAEKQFKEKPSKHFSEWEDIVRW 299
Db 241 MSRAVEQAAPWLILVSGGDIADVLAAALVNQPHLLVPQVTEKQFKEKPSSECFSEWAIHVW 300
QY 300 TKLLQNTSHOHLITVYDFEQSGSELDVTILKALVKACKSHSQSPQDYLDLKLAVWD 359
Db 301 TELLQNTIAHPHLLITVYDFEQSGSELDVTILKALVKACKSHSROAQDYLDLKLAVWD 360
QY 360 RVDIAKSEIFNGDVENKSCDLEEVMDALVSNKPEFVRLFVNGADVADFLTYGRLOELY 419
Db 361 RVDIAKSEIFNGDVENKSCDLEEVMDALVSNKPEFVRLFVDSGADMAEFITYGRLOELY 420
QY 420 RSVSRKSLFLDLQKQKOEARELTLAGLGTQOAREPPAGPPAFSLHEVSRVLKDFLODADR 479
Db 421 HSVSPKSLFLDLQKQKOEARELTLAGLGTQOAREPPAGPPAFSLHEVSRVLKDFLODADR 480
QY 480 GFYQDGRPGDRRAEKGPAKRTGQKWLJDNOKSENPMRDILFWAVLQNRHEMATYPWA 539
Db 481 GFYQDGRPGDRRAEKGPAKRTGQKWLJDNOKSENPMRDILFWAVLQNRHEMATYPWA 536
QY 540 MQQGVAAALAAACKILKEMSHLETAABARAAREAKYERLALDLFSECVSNSEARAFALL 599
Db 537 MGRGVAAALAAACKILKEMSHLETAABARAAREAKYERLALDLFSECVSNSEARAFALL 596
QY 600 VRNRCSWSTTCLHATEADAKAFPAHDGVQAFLTRIWWGDMAGTPTILRLGAFGLCPAL 659
Db 597 VRNRCSWSTTCLHATEADAKAFPAHDGVQAFLTRIWWGDMAGTPTILRLGAFGLCPAL 656
QY 660 VYTNLITFSEAPLTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQDGRPAVF 719
Db 657 VYTNLITFSEAPLTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQDGRPAVF 716
QY 720 LLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPPQSGPSEVTLFWFVTLV 779
Db 717 LLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPPQSGPSEVTLFWFVTLV 776
QY 780 LLEIRQGFPTDEDTHLVKFTLYVGDNNKCDMAIFLFIIVGVTCTRMPLPSAPEAGRTVLA 839
Db 777 LLEIRQGFPTDEDTHLVKFTLYVGDNNKCDMAIFLFIIVGVTCTRMPLPSAPEAGRTVLA 836
QY 840 MDMVFTLRLIHI FAIHKQLGPKIIVVERMMKDVFFFLFVSWLVAYGVTTQALLHPHD 899
Db 837 IDFMVFTLRLIHI FAIHKQLGPKIIVVERMMKDVFFFLFVSWLVAYGVTTQALLHPHD 896
QY 900 GRLEWIFRVLRYRPLQIFQGIPIDEIDEARVNGSTHPLLEDSPSCPSIYANWLILL 959
Db 897 GRLEWIFRVLRYRPLQIFQGIPIDEIDEARVNGSTHPLLEDSPSCPSIYANWLILL 956
QY 960 VTFLLVNVLNMLLIAMFSYTFVQGNADMFWMKFORYNLIYVEYHERPALAPFTILSH 1019
Db 957 VTFLLVNVLNMLLIAMFSYTFVQGNADMFWMKFORYNLIYVEYHERPALAPFTILSH 1016
QY 1020 LSLTLRRVFKAEHKEHLEERDLPDLPDQKVVTWETVQKENFSLKMKERRRDESEVLR 1079
Db 1017 LSLTLRRVFKAEHKEHLEERDLPDLPDQKVVTWETVQKENFSLKMKERRRDESEVLR 1076

QY 1080 KTAHRVDIAKYIGLREQEKRIKLESQINYSVSVADVLAQGGPRSSQHCCEGS 1139
Db 1077 KTAHRVDIAKYIGLREQEKRIKLESQINYSVSVADVLAQGGPRSSQHCCEGS 1136
QY 1140 QLVAAHRRGLDGEQPGAGOPPSDT 1165
Db 1137 QPASARDREYLE-----AGLPHSDT 1156

RESULT 12
US-10-026-188-2
; Sequence 2, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yifeng
; APPLICANT: Zuker, Charles S.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat L-TRP taste predicted protein
US-10-026-188-2

Query Match      82.2%; Score 5008.5; DB 13; Length 1165;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 965; Conservative 77; Mismatches 113; Indels 11; Gaps 3;

QY 1 MDVQGPDPGSGDAEDRRLGLHGEVNFVGGSGKRGKRVPSGVAPSVLFDLLLAEW 60
Db 9 MPMAQSSCPGSPDPTDGDWEVLCKEGVNFVGGSGKSKFVKVPSNVAPSMLELLLTW 68
QY 61 HLPAPNLVSVLGEVQPFAMKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGOAV 120
Db 69 HLPAPNLVSVLGEERLFAKMSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGOAV 128
QY 121 RDHSLASTSTKVRVAVGMSASGLRVLRHRLLEAEQEDFPVHYPEDDGGSGPLCSLDSNL 180
Db 129 RDHSLASTSTKVRVAVGMSASGLRVLRHRLLEAEQEDFPVHYPEDDGGSGPLCSLDSNL 188
QY 181 SHFILVPEPTLGSNDGLAEQLSLEKHSQRTGYGTSIQIPVLCLLVNGDPSTLER 239
Db 189 SHFILVPEPTLGSNDGLAEQLSLEKHSQRTGYGTSIQIPVLCLLVNGDPSTLER 248
QY 240 ISRAVEQAAPWLILVSGGDIADVLAAALVNQPHLLVPKVAEKQFKEKPSKHFSEWEDIVRW 299
Db 249 MSRAVEQAAPWLILVSGGDIADVLAAALVNQPHLLVPQVTEKQFKEKPSSECFSEWAIHVW 308
QY 300 TKLLQNTSHOHLITVYDFEQSGSELDVTILKALVKACKSHSQSPQDYLDLKLAVWD 359
Db 309 TELLQNTIAHPHLLITVYDFEQSGSELDVTILKALVKACKSHSROAQDYLDLKLAVWD 368
QY 360 RVDIAKSEIFNGDVENKSCDLEEVMDALVSNKPEFVRLFVNGADVADFLTYGRLOELY 419
Db 369 RVDIAKSEIFNGDVENKSCDLEEVMDALVSNKPEFVRLFVDSGADMAEFITYGRLOELY 428
QY 420 RSVSRKSLFLDLQKQKOEARELTLAGLGTQOAREPPAGPPAFSLHEVSRVLKDFLODADR 479
Db 429 HSVSPKSLFLDLQKQKOEARELTLAGLGTQOAREPPAGPPAFSLHEVSRVLKDFLODADR 486
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QY 480 GYQDGRPCDERRAEKGPAPKRTGOKWLLDLNOKSENPRDLFLWAVLQNRHEMATYFWA 539
DB 489 GYQDGRPCDERRAEKGPAPKRTGOKWLLDLNOKSENPRDLFLWAVLQNRHEMATYFWA 544
QY 540 MQQEGVAAALAAACKILKEMSHLETAEAAATREAKYERLALDLFSECYNSSEARAFALL 599
DB 545 MGRGVAAALAAACKILKEMSHLEAEAVARTREAKYEQALDLFSECYNSSEARAFALL 604
QY 600 VRRNRCWKTCTCHLATEADAKAFADHGVQVFLTRIWMGDMAGTPIRLILGALCPAL 659
DB 605 VRRNHSWRTCTCHLATEADAKAFADHGVQVFLTRIWMGDMATGPIRLILGALCPAL 664
QY 660 VYTNLITSEAPLRTGLDLOLSDTEKSPLYGLOSRRVEELVEAPRAQDGRPAVF 719
DB 665 IYTNLITSEAPLRTGLDLOLSDTEKSPLYGLOSRRVEELVEAPRAQDGRPAVF 724
QY 720 LTRWRKFWGAPVTVFLGNVVMYFAPLFTYVLLVDFRPPQSGSEVTVLYFWVFTLV 779
DB 725 LTRWRKFWGAPVTVFLGNVVMYFAPLFTYVLLVDFRPPQSGSEVTVLYFWVFTLV 784
QY 780 LEEIRQGFPTDTHLVKFTLYVGNWNNKCDMVAIFLIVGVTCTRMPLPSAEAGRTVLA 839
DB 785 LEEIRQGFPTDTHLVKFTLYVGNWNNKCDMVAIFLIVGVTCTRMPLPSAEAGRTVLA 844
QY 840 MDPMVFTLRLLIHFATHKOLGPKIIVVERMKDVPFFLFLSVLWVAYGVTTQALLPHD 899
DB 845 IDPMVFTLRLLIHFATHKOLGPKIIVVERMKDVPFFLFLSVLWVAYGVTTQALLPHD 904
QY 900 GRLEWIFRVLRYPLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILL 959
DB 905 GRLEWIFRVLRYPLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILL 964
QY 960 VTFLVNTVLLNMLLIAMSYTFQVQGNADFWKFORNLIVEHERPALAPPTLLSH 1019
DB 965 VTFLVNTVLLNMLLIAMSYTFQVQGNADFWKFORNLIVEHERPALAPPTLLSH 1024
QY 1020 LSLTLRRVFKAEHKEHLEHRLDPLDQKVVTWETVOKENFLSMKRRRDSSEVL 1079
DB 1025 LSLTLRRVFKAEHKEHLEHRLDPLDQKVVTWETVOKENFLSMKRRRDSSEVL 1084
QY 1080 KTAHRVDFTAKYGLGRLREKRIKLESQINYCSVLVSSVADYLAQGGPRSSQHCGES 1139
DB 1085 KTAHRVDFTAKYGLGRLREKRIKLESQINYCSVLVSSVADYLAQGGPRSSQHCGES 1144
QY 1140 QLVADHRGGLDQWQFQAGQPPSDT 1165
DB 1145 QPASARDREYLE-----AGLPHSDT 1164

RESULT 13
US-10-295-027-558
; Sequence 558, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; APPLICANT: Eos Biotechnology, Inc.
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 558
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-558

Query Match 40.2%; Score 2448.5; DB 15; Length 1166;
Best Local Similarity 45.6%; Pred. No. 1.5e-202;
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

QY 26 GEVNGGSGKRGKRVVPSPVAPSVLFDLLAEHHLAPNLVSLVSGEOPFAMKSWLR 85
DB 28 GELDTGAGRKHSNFRSLSDRTDPAAYSLVTRTWGFRAPNLVSLVSGGSGPVLTQWLQ 87
QY 86 DVLRLGLVKAQOSTCAWILTSAIRVGLARHVGQAVRDHSLASTSTKRVVAVGMAISLGRV 145
DB 88 DLLRLGLVRAQOSTCAWILTSAIRVGLARHVGQAVRDHSLASTSTKRVVAVGMAISLGRV 146
QY 146 LHRRLILEBAQEDFPVHY-----PEDDGGSGQLCSLSDNSLHFLVPEGPPGKGDGLTEL 200
DB 147 RNRDLINPKGSPFARYWRGDPED--GVQFP--LDYNSAFFLVDDGTHGCLGGENRF 201
QY 201 RLRLEKHISEQAGYGGTGSIBIPVCLLVNDGPTLRIERISRAVEQAAPWLLVSGSGTA 260
DB 202 RLRLESYISQQTGVGGTG-IDIPVLLLLIDGDERMLTRIENATQALPCLLVSGSGAA 260
QY 261 DVLAALVNPQLLVP-----KVAEQPKFKFPSPKHSFWSWEDIVRWTKLLQNTSHOHL 313
DB 261 DCLAETLED--TLAPGSGGARQGEARDRIIRFPFK-----GDLEVLQAOVERIMTRKELL 313
QY 314 TVYDFEQSGSEHLDTVILKALVKACKSHSQBPQDYLDELKLAVAWDRVDIAKSEIFNGDV 373
DB 314 TVYSSE-DGSEEFETIVLKVAC--GSSEASAVILDELRLAVANWVVDIAQSELPRGDI 370
QY 374 EWKSCDLEEVMDALVSNKPEFVFLVNDGADVADFLTYGRLOELYRSVRKSLFLDLIQ 433
DB 371 QWRSPHLEASLMDALLNDRPEFVRLIISHGLSHFLTPMRLAQYLSAAPSINRLNLD 430
QY 434 RKQEEARLTLAGL--GTQQAAREPPAGPPAFSLHESVRLKDFLQDACRFQYDGRPCDRR 491
DB 431 QASHSAGTKAPALKGGAELRPP-----DVGHVLRMLLKGKVCAPRYPYSGGAWDPH 480
QY 492 RAEKGPAPKRTGOKWLLDLNOKS-----ENPWRDLFLWAVLQNRHEMATYFWAMGQ 542
DB 481 -----PQQFGESWYLLSDKATSPSLDAGLQAPWSDLLWALLNRAQMAFYFWMGMS 535
QY 543 EGVAAALAAACKILKEMSHLETAEAAATREAA--KYERLALDLFSCYNSSEARAFALL 600
DB 536 NAVSSALGACLLLRVMARLEPDAEEAARRKOLAFKEGMDVLFGEBCYRSESVRAARLL 595
QY 601 RNRWCWKTCTCHLATEADAKAFADHGVQVFLTRIWMGDMAGTPIRLILGALCPALV 660
DB 596 RRCPLMGDATCLOLQAMQADARAFFAQDGVQSLTQKWMGDMASTTPIWLVLVAFPCPLI 655

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QY 661 YTNLITF--SEEAPLRTGLELDQLDLSLDTSEKSPGLYQSRVEELVEAPRAQD----- 712
Db 656 YTNLITFRKSEETREELE--FDMSVINGEGVGTADPAEKTPLGVPRQSGRPGCCGG 713
QY 713 --RGPRAVFLTLTRKFWGAPVTVFGNVVMPAPFLFTYVLLVDFRPPQPSGPEVT 770
Db 714 RCGGRRC--LRWFHFWGAPVTFMGNVVSVLLFLLFSRLLVDFQFAP--PGSLELL 768
QY 771 LYFWVFTLVLEIRQGFDTDEDT-----HLVKKFTLYVGDNNKCDMVAIFPI 819
Db 769 LYFWAFTLLCEELRQGLSGGSLASGGPGPHASLSQRLRLYLADSNQCDLVALTCFL 828
QY 820 VGYTCRMLPSAFEGAGRTVLAMDFMFTLRLIHFAHKLQKGLIIVVERMMKDVFFFLFF 879
Db 829 LGVGCRLTGLYHLGRVLCIDFMFTVTELLHFTVKNQKGLKIVIVSKMKDKVFFFLFF 888
QY 880 LSWLVAYGVYVQALLPHDGRLEWIFRVLVRYPIQIGQIPLDEIDEARV---NCSTH 936
Db 889 LGVWLVAVGATEGLLRPRDSDFPSILRVFVRVYPIQIPQDMDVLMHEHNSCSSE 948
QY 937 PLLLEDSP-----SCPSLVANMLVILLVTFILLVNTNLLMLLIAMFSYTFQVQGNADM 991
Db 949 PGFWAHPGAQAGTCVSQYANMLVILLVIFLLVANILLVNLIIAMFSYTFQVQGNADL 1008
QY 992 FWKFORNLIVYHERPALAPPFILLSHLSLTLRVFKK-----EAEHKREHLERD 1042
Db 1009 YNKAQRYRLIREFHSRPAALAPPFIVISHLRLRLQLCRRPSPQSPSALAEHFRVLYSKE 1068
QY 1043 LPDPLDQKVWVETQKFNFLSKMKRRRDSGEVLRTAHRVDVFIKYLGLRQEKRI 1102
Db 1069 ----AERKLLTWESVHKFNFLARARAKRESERLKRTSQKVDIALQKLGHIHREYQRL 1124
QY 1103 KCLESQINVCVLSVSSADVLAQG-----GGP 1129
Db 1125 KVLREVQCCSRVLCGWAEALSRSALLPPGGP 1156

RESULT 14
US-10-295-027-916
; Sequence 916, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
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; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 916
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-916
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Query Match 40.2%; Score 2448.5; DB 15; Length 1166;
Best Local Similarity 45.6%; Pred. No. 1.5e-202;
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

QY 26 GEVNFSGGKRGKRVFVPSGVAPSVLFDLLAEWHLPAPNLVSVLGEQPFAMKSWLR 85
Db 28 GELDTGAGRKHSNFLRLSDRTDPAAYSLVTRTWGFRAPNLVSVLGGSGGPVLQTLQ 87
QY 86 DVLRKGLVKAQAQSTGAWILTSALRVGLARHVGQAVRDHSLASTSTKVRVAVGMASLGRV 145
Db 88 DLLRGLVRAAQSTGAWIVTGLTGLGRHVGVAVRDHQAATG-GTKVVAVGVAPGVV 146
QY 146 LHRRIIEAQBDFPVHY-----PEDDGGSGQPLCSLDSNLSHFILVEPPGKDGTEL 200
Db 147 RNRDTLNPKGSPFARYRWGDPED--GVQFP---LDYNSAFPLVDGTHGCLGGENRF 201
QY 201 RLRLKHSISQAGYGGTGSIEIPVLCLLVGNPDNTERISRAVEQAAPWLILVSGGGIA 260
Db 202 RLRLSVISQKTVGGGTG-IDIPVLLLDIGDEKMLTRIENATQAQLPCLLVAGSGGAA 260
QY 261 DVLAALVNQPHLLVP-----KVAKQPKKEKPPSKHFSWEDIVRWTKLQNTTSHQLL 313
Db 261 DCLAETLED--TLAPGGGARGEARDRIRRPFPK-----GDLEVLQAQVERIMTRKELL 313
QY 314 TVYDFPQEGSEELDTVLKALKVAKSKHQEPQDYLDLKLAVMDRVDIAKSEIFNGDV 373
Db 314 TVYSSE-DGSEEPETVLKALKVAK--GSSEASAYLDELRLAVAMNRVDIAQSELFRGDI 370
QY 374 ENKSCDLEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOQLYRSVSRKSLPDLQ 433
Db 371 QWSEFHLASLMDALLNDRPEFVRLIISHGLSLGHFLTPMRLAQLYSAAPSNSLRNLLD 430
QY 434 RKOEEARLTLAGL--GTQOAREPPAPPAFSLHESVRLKDFLQDACRGFYQDGRPGRR 491
Db 431 QASHSAGTKAPALKGGAAELRPP-----DVGHVLRMLLIGKMCAPRYPSGGAWDPH 480
QY 492 RAEKGPAKRPTGQKWLILLNQS-----ENPRDLFLNAVLRNHEMATYFWAMCQ 542
Db 481 -----PQGFSGSMYLLSDKATSPSLDAGLQAPWSDLLWALLLNRAQMAFYFWMGS 535
QY 543 EGVAAALAAACKILKEMSHLETAEARATREA--KYERLALDLFSECYNSBARAPALIV 600
Db 536 NAVSSALGACLLLRVMARLEPDAEEAARRKDLAFEGEGVDLPGEICYSSEVRAARLL 595
QY 601 RNRCSKTTCLHATEADAKAFPAHDGVOAFLTRWGDMAAGTPIELLLGAPICPALV 660
Db 596 RRCPLMGDTCIQLAMQADARAPFAQDGVOSLLTKQWGDMASTTPIWALVLAFFCPPLI 655
QY 661 YTNLITF--SEEAPLRTGLELDQLDLSLDTSEKSPGLYQSRVEELVEAPRAQD----- 712
Db 656 YTNLITFRKSEETREELE--FDMSVINGEGVGTADPAEKTPLGVPRQSGRPGCCGG 713
QY 713 --RGPRAVFLTLTRKFWGAPVTVFGNVVMPAPFLFTYVLLVDFRPPQPSGPEVT 770
Db 714 RCGGRRC--LRWFHFWGAPVTFMGNVVSVLLFLLFSRLLVDFQFAP--PGSLELL 768
QY 771 LYFWVFTLVLEIRQGFDTDEDT-----HLVKKFTLYVGDNNKCDMVAIFPI 819
Db 769 LYFWAFTLLCEELRQGLSGGSLASGGPGPHASLSQRLRLYLADSNQCDLVALTCFL 828
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QY 820 VGVTCRLMPSAFAGRTVLAMDVMVFTLRLIHIHFAIHKQLGPKIIVVERMKDVFVFFLF 879
 DB 829 LGVGCRLTPGLYHLGRTVLCIDFMVFTVRLHLIHTVVKQLGPKIVIVSKMKDVFVFFLF 888
 QY 880 LSVMLVAYGVTTQALLPHDGRLEWIFRRVLYRYPYLOIFGOIPDLDEIDARV---NCSTH 936
 DB 889 LGVMLVAYGVATGELLRPDSDFPSILRRVYRYPYLOIFGOIPQEDMDVALMEHSNCSE 948
 QY 937 PLLLEDSP-----SCPSLYANWLVLLAVTLLVNTVLLMNLIIAMFSYTFQVQGNADM 991
 DB 949 PGFWAHPFGAAGTCVSOYANWLVLLVIFLLVANILLVNLIIAMFSYTFQVQGNADM 1008
 QY 992 FWKFORYNLIVEYHERPALAPPFILLSHLSLTLRVFKK-----EAEHKREHLERD 1042
 DB 1009 YWKAQRYLIREFHSRPPALAPPFIVISHLRLQLCRRPRSPQSSPALEHFRVYLSKE 1068
 QY 1043 LPDPLDQKVVTWETVOKENFLSKMKRRRDSGEVLRKTAHRVDFTIAYKLGRLRBOEKRI 1102
 DB 1069 ---AERKLLTWESVHKNFLLARADKRESDSERLKRKTSOKVDLALKOLGHIREYEQRL 1124
 QY 1103 KCLESQINYCSVLVSSVADVLAQG-----GGP 1129
 DB 1125 KYLEREVQOCRSVLGWVAEALSALLPPGGP 1156

RESULT 15
 US-10-142-649-2
 ; Sequence 2, Application US/10142649
 ; Publication No. US20030143557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penner, Reinhold
 ; TITLE OF INVENTION: Methods of Screening for TRPM4b Modulators
 ; FILE REFERENCE: A-71325-2/RFT/NBC
 ; CURRENT APPLICATION NUMBER: US/10/142,649
 ; CURRENT FILING DATE: 2002-10-02
 ; PRIOR APPLICATION NUMBER: 60/351,938
 ; PRIOR FILING DATE: 2002-01-25
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1214
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-142-649-2

Query Match 40.2%; Score 2448.5; DB 14; Length 1214;
 Best Local Similarity 45.6%; Pred. No. 1.6e-202;
 Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

QY 26 GEVNFQGGKGRKGFVRVPSGVAPSVLFDLLAEWHLPAIHLVSVLGVGEQPFAMKSWLR 85
 DB 76 GELDFTGAGRGHNSFLRLSDRTDPAAYSLVTRTWGFRAPNLVSVLGGSGGPGVLTWLQ 135
 QY 86 DVLKGLVAAQSTGAWILTSALRVGLARHVGOAVRDHSLASTSTKRVVAVGMAASLGRV 145
 DB 136 DLLRRGLVRAAQSTGAWIVTGHLTGIRHVGAVARDHQAQSTG-CTKVVAVGVAWGVV 194
 QY 146 LHRRIILEEAQEDFPVHY-----PEDDGGSGGPGVLCSDLSNLSHFILVPEGPPGKGDGLTEL 200
 DB 195 RNRDRLINPKGSPFARYRWGDPED--GVQFP--LDVYNSAPFLVDDGTHGCLGGENRF 249
 QY 201 RLRLKXHSIQRAGYGGTGSIEIPVLCLLVNGDPNTLIRISRAVEQAAPWHLILVGGGGA 260
 DB 250 RLRLSYISQKGTGVTG-IDIPLVLLLDGDERKMLTRIENATQAQLPCLLVAGSGGA 308
 QY 261 DVLAALVNQPHLLVP-----KVAEQKPEKFPKSHFSDIVRWTKLQNTITSHOHL 313
 DB 309 DCLAETLED---TLAPSGGARQGEARDIRIRFPK-----GDLEVLQAQVERIWTWKELL 361
 QY 314 TVYDFEOGSEELDTVLKALVKACKSHSQEPQDYLDELKAVAWDRVDIAKSEIFNGDV 373
 DB 362 TVYSSE-DGSEEFETIVKALVKAC--GSSEASAYLDELAVAMNRVDIAQSELFRGDI 418

QY 374 EWKSCDLEWVNDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYSVSRKSLFDLLQ 433
 DB 419 QWRSFHLEASIMDALLNDPEFVRLIISHLGSLGHFTLPMRLAQLYSAAPSNSLIRLLD 478
 QY 434 RKQEARLTLAGL--GTQOAREPPAGPPAFPSLHSEVSVLQDFLQDACRGFFQDGRPGDRR 491
 DB 479 QASHSAGTKAPALKGGAAELRPP-----DVGHVLRMLLGMKCAPRYPSSGAWDPH 528
 QY 492 RAEGKPAKRPRTGQKWLDDLNQKS-----ENPWRDLFLWAVLQNRHEMATYFWAMQ 542
 DB 529 -----PGGFGESWYLLSDKATSPLSLDAGLQAPWSDLLIALLLWALLNRAQWAMFWEMGS 583
 QY 543 EGVAAALAAACKILKEMSHLETEAARATREA--KYERLALDLPSECVSSEARAFALLV 600
 DB 584 NAVSSALGACLLLRVMALEPDAEAAARKDLAFKFGMGVDLFGECYRSEARARULL 643
 QY 601 RNRCSWKTTCCLHATADAKAPFAHDGVOAFTRIMWGDMAAGTPIILRLGAFCLPALV 660
 DB 644 RRCPLMGDATCLQAMQADARAFFAQDQVQSLLTQKWWGDMASTTPIWALVLAFCPPLI 703
 QY 661 YTNLITF--SEEAPLRTGLEDLQDLSLDTEKSPLYGLQSRVEBELVEAPRAQGD----- 712
 DB 704 YTRLITFKSEETRELE--FDMDSVINGEGPVGTADPAEKTPLGVPRQSGRGCCGG 761
 QY 713 --RGPRVFLLTRWRKFWGAPVTVPLGNVVMYFAFLFTVTVLLVDFRPPQGGSGPEVT 770
 DB 762 RCGGRRC---LRRWFHFWGADVTIFMGNVVSYLLFLLFSRVLLVDFQAP--PGSLELL 816
 QY 771 LYFWVFTLVLEIRQGFPTDEDT-----HLVKFTLYVGDNNKNCMDVAIFLPI 819
 DB 817 LYFWAFTLLCBELRQGLSGGGSLASGGPGGCHASLSORLRLYLADSNNQCDLVALTCFL 876
 QY 820 VGVTCRLMPSAFAGRTVLAMDVMVFTLRLIHIHFAIHKQLGPKIIVVERMKDVFVFFLF 879
 DB 877 LGVGCRLTPGLYHLGRTVLCIDFMVFTVRLHLIHTVVKQLGPKIVIVSKMKDVFVFFLF 936
 QY 880 LSVMLVAYGVTTQALLPHDGRLEWIFRRVLYRYPYLOIFGOIPDLDEIDARV---NCSTH 936
 DB 937 LGVMLVAYGVATGELLRPDSDFPSILRRVYRYPYLOIFGOIPQEDMDVALMEHSNCSE 996
 QY 937 PLLLEDSP-----SCPSLYANWLVLLAVTLLVNTVLLMNLIIAMFSYTFQVQGNADM 991
 DB 997 PGFWAHPFGAAGTCVSOYANWLVLLVIFLLVANILLVNLIIAMFSYTFQVQGNADM 1056
 QY 992 FWKFORYNLIVEYHERPALAPPFILLSHLSLTLRVFKK-----EAEHKREHLERD 1042
 DB 1057 YWKAQRYLIREFHSRPPALAPPFIVISHLRLQLCRRPRSPQSSPALEHFRVYLSKE 1116
 QY 1043 LPDPLDQKVVTWETVOKENFLSKMKRRRDSGEVLRKTAHRVDFTIAYKLGRLRBOEKRI 1102
 DB 1117 ---AERKLLTWESVHKNFLLARADKRESDSERLKRKTSOKVDLALKOLGHIREYEQRL 1172
 QY 1103 KCLESQINYCSVLVSSVADVLAQG-----GGP 1129
 DB 1173 KYLEREVQOCRSVLGWVAEALSALLPPGGP 1204

Search completed: June 22, 2005, 18:33:14
 Job time : 183 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 18:08:59 ; Search time 50 seconds
(without alignments)
2241.851 Million cell updates/sec

Title: US-09-834-792D-4
Perfect score: 6093
Sequence: 1 MQDVQPRPGSGDAERRE.....HRGGLDGWEQPGAGQPPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl2: *
3: Pirl3: *
4: Pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1134.5	18.6	488	JC7995	transient receptor
2	1070.5	17.6	1868	T23707	hypothetical prote
3	1000	16.4	1400	T22644	hypothetical prote
4	899	14.6	1707	T18951	hypothetical prote
5	326.5	5.4	1275	JU0092	trp protein - frui
6	317.5	5.2	1274	JN0015	trp protein - frui
7	294	4.8	1418	S40764	hypothetical prote
8	266.5	4.4	1124	JH0588	calmodulin-binding
9	247	4.1	899	F88391	protein R06B10.4
10	235.5	3.9	823	S44873	ZC21.2 protein - C
11	192	3.2	828	JC5807	trp3 protein - rat
12	176.5	2.9	793	S68238	trp1 protein - hu
13	176.5	2.9	810	T38361	TRPC1 protein - hu
14	165	2.7	823	T34472	hypothetical prote
15	164.5	2.7	3678	S28912	dystrophin - mouse
16	160.5	2.6	482	S61648	probable membrane
17	146	2.4	725	JC7531	calcium transport
18	145.5	2.4	675	T20822	hypothetical prote
19	144.5	2.4	839	JC7621	capsaicin receptor
20	139	2.3	727	JC7796	epithelial calcium
21	132	2.2	790	T20312	hypothetical prote
22	130	2.1	838	T09054	capsaicin receptor
23	130	2.1	2049	T43161	sodium channel pro
24	128	2.1	723	JC7795	epithelial calcium
25	128	2.1	900	T33026	hypothetical prote
26	124.5	2.0	608	G02640	polycystic kidney
27	123.5	2.0	1199	T37561	probable transcrip
28	123	2.0	1060	S63993	acrosomal protein
29	123	2.0	1075	T45570	kinesin-like prote

ALIGNMENTS

RESULT 1

JC7995
transient receptor potential-melastatin 4 channel - mouse

C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C:Accession: JC7995
R:Murakami, M.; Xu, F.; Miyoshi, I.; Sato, E.; Ono, K.; Iijima, T.
Biochem. Biophys. Res. Commun. 307, 522-528, 2003
A:Title: Identification and characterization of the murine TRPM4 channel.
A:Reference number: JC7995; PMID:12893253
A:Accession: JC7995
A:Molecule type: DNA
A:Residues: 1-488 <MUR>
A:Cross-references: GB:NM000319
A:Experimental source: Brain, C57/BL6
C:Comment: This protein, a member of subfamily of transient receptor potential channels
C:Genetics:
A:Gene: trpm4

A:Map position: 782
A:Introns: 12/2; 153/2; 197/3; 256/1; 315/2; 384/1; 428/2; 452/3
C:Keywords: calcium entry; transient receptor potential; transmembrane domain; TRPM

Query Match	18.6%;	Score 1134.5;	DB 2;	Length 488;	
Best Local Similarity	47.6%;	Pred. No. 1.6e-74;			
Matches	236;	Conservative 72;	Mismatches 123;	Indels 65; Gaps 10;	
QY	704	VEAPRAQGRGPRAPV---	LLTRWRKFWGAPVTVLGNVVMYFAFLFTYLLVDFRPP	760	
DB	20	VALERRRRRPGRCALCCGKFKRWSDFWGPVTAFLGNVSYLLFLLFAHLLVDFQPT	79		
QY	761	POGSPGPEVTLFYWVFTLVLEIRGQF-----	FTDEDTHLVKKFTLYVGDNNWK	809	
DB	80	K--PSVSELLLYFNAFTLLCEBLRQGLGGGWSGLASGGRGPDAPLRHRLHLYLSDTNQ	137		
QY	810	CDWVAIFLIVGVTCHMLPSAFAEAGRTVLAMDPMVFTLRIHIFAIHKGKPKIIVVERM	869		
DB	138	CDLLALTCLFLGVGCELTGLFDLGTVLCLDFMIFTLRLHIFTVKNQKQKIVIVSKM	197		
QY	870	MKDVFVFFFLSVLWVAYGVTTQALLPHDGLKLEWIFRRVLYRPLYQIFGQPLDEIDEA	929		
DB	198	MKDVFVFFFLSVLWVAYGVATEGILRPQDRSLPSILRRVFRVRYLYQIFGQIPQEBMDVA	257		
QY	930	RV-----NCS-----	THPLLEDSP---	SCPSLYANWLVLVLTLLVNTNLLMLLIAM	977
DB	258	LMIPGNCMSMERGSAHP-----	EGPVAGSCVQYANWLVLVLTLLVNTNLLMLLIAM	313	
QY	978	FSYTFQVQGNADMFWKFORNLYVEYHERPALAPFILLSHLSLTLR-----	RVFK	1029	
DB	314	FSYTFQVQGNADMFWKFORNLYVEYHERPALAPFILLSHLSLTLR-----	RVFK	1029	
QY	1030	KEAHEKREHLERLDPDLPDQKVVTWETQKFNFLSKMEKRRRDSGEVLKRTAHRVDFIA	1089		

Db 374 LPASPVPFPRVCLSKAEAKLLTWESVHKENFLLAQAKRDSERLKRSTQKVDYAL 433
 Qy 1090 KYLGLREDEKRIKICLESQINYSVLVSSVADVLAQGGPRSSQHCGBGSQSLVADHGG 1149
 Db 434 KQLGQIREYDRRLRGLEREVOHCSRLVTWAEALSH-----SALL----- 473
 Qy 1150 LDGWEQFGAGQPPSDT 1165
 Db 474 -----PPGAPPPPSPT 484
 RESULT 2
 T23707
 hypothetical protein T01H8.5 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T23707; T24342
 R;Kerhaw, J.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19786
 A;Accession: T23707
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1868 <WIL>
 A;Cross-references: EMBL:Z83117; PIDN:CAB05572.1; GSPDB:GN00019; CESP:T01H8.5
 A;Experimental source: clone M04C7
 R;Lennard, N.
 submitted to the EMBL Data Library, September 1996
 A;Reference number: Z19877
 A;Accession: T24342
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1868 <W12>
 A;Cross-references: EMBL:Z80219; PIDN:CAB02303.1; GSPDB:GN00019; CESP:T01H8.5
 A;Experimental source: clone T01H8
 C;Genetics:
 A;Gene: CESP:T01H8.5
 A;Map position: 1
 A;Introns: 24/3; 112/3; 191/3; 220/1; 268/2; 375/2; 456/2; 552/3; 625/2; 744/3; 850/2; 1
 Query Match 17.6%; Score 1070.5; DB 2; Length 1868;
 Best Local Similarity 24.5%; Pred. No. 5.7e-69;
 Matches 343; Conservative 231; Mismatches 486; Indels 341; Gaps 41;
 Qy 26 GEVNF-GSGKKRGKFRVPSPGVAPSLFLDLAELWHPAPNLVSLVGBEQPFAMKSL 84
 Db 214 GQVEFGGPHPYKQYVRVNPTEPAYTMSLFHVWQISPRLLIIVHGGTSNFDLQPKL 273
 Qy 85 RDLRKGLVKAQSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGNASLGR 144
 Db 274 ARVFRKGLLKAASTTGAWIITSGCDTGVVGVHVAALLEG---AQSAQRNKIVCIGIAPWG- 329
 Qy 145 VLHRLIREAQEDF-----PVHYEDDGGGQGPLCLSDLSNLSHFILVPPGPKGDGLT 198
 Db 330 -----LUKKREDFGQDKTVPYYP---SSKGRFTGLNNRHSYFLLVNDGTVGRYGAEV 380
 Qy 199 ELRLKELHISQRAYGGTGSIEIPVLCLVNGDPNTERISRAVEQA---APWLILVGS 256
 Db 381 ILRKELEWISQKQIFGGTRS---VPVVCVVLGGSCITIRSDYVTVNVPVPPVVCDS 438
 Qy 257 GGIADVLAAL---VNQPHLL-----VPKVAEQKPKFKPSKHSFWMEDIVRWTKLLQNI 306
 Db 439 GRAADLAFAHQNVTEDEGLLPDDIRRQVLLLVETTFGCEAAAH-----RLHHEL 488
 Qy 307 T---SHOHLTVYDFEQRSGSELDVTILKALVKACKSHSQBPQDYLDLKLAVAWDRVDI 363
 Db 489 TVCAQKNLLIFRLGEGEHDVDAITALKG-----QNLGAADQLALAAWNRVDI 542
 Qy 364 AKSEIFNGDVWKSCDLEEVVMDVLVSNKPEFVRLFVDNGADVADFLTYGRLOELY---- 419
 Db 543 ARSDVFAMGHEWPPQAAALHANMAEALIHDRVDFVRLLEQGINMQKFLTISRDLDELNTDK 602
 Qy 420 -----RSVSRK-----SLLPDLL-----QRKQEEARL- 441

RESULT 3

T22644

hypothetical protein F54D1.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

Db 603 GPPNTLFYIVRDVVRVQGYRFLKPLDGLVIEKLMGNSYQCSYTTSEBFRKQKMRKV 662
 Qy 442 -----TLAGLGTQARE-----PPAGPPA-F 461
 Db 663 HAQKAMGVFSSRSRSTGSGIASRQSTEGMGVGGSSVAGVFGNSFGNQDPPLDPHVNR 722
 Qy 462 SLHEVSRVLKDFL--QDACRGFYQDGRPGDRAEAKGPAKRPQTQKWLILLNKSEN--- 516
 Db 723 SALSGRALSNNHILWRSAFRGNF---PANPMRPNLGDSDGSEBDELSLTSADGS 778
 Qy 517 -----PWEDLFWAVLQNRHEMATYFWAMGQEGVAAALAAACKILKENS-----HLE 562
 Db 779 QTEPDFRYPYSELMIWAVLTKQDMAMCMQWQHEEAMAKALVACRLYKSLTAEEADYLE 838
 Qy 563 TEAABARATREAKYERLALDLFSECYSNSBARAFALLVRRNRCSWTKTCLHLHATEADA 622
 Db 839 VEICEELKYAEPRILLSLELDHCHYHDDAQTLLTYELSNWSNETCLALAVVNNKH 898
 Qy 623 FFAHDGVQAFTRIWMGDMAGT--PILRLLAGFLCPALV----- 660
 Db 899 FLAHPCCQILLADLWHGGLRMRTSHNIKVVVLGLICPPFIQMLEFKTREELINQPTAAEH 958
 Qy 661 -----YTNLITFGEAPLRTGLEDLQDLSLDE----- 689
 Db 959 QNDMNYSS 1018
 Qy 690 ----- 699
 Db 1019 LFHSRRKAKNEKCDRETDASACEAGNRQIQNGGLTAEGTGTGESNGVSPPPPYMRANS 1078
 Qy 690 -----KSPLYGLQSRVEELVEAPRAQGR-----GPRAVFLTRWRKFW 728
 Db 1079 RSRYNNSDMSTSSVIFGSDPNLSKLOKSNIITSDRPNPMEQFOGTRKIKMRRRYEYF 1138
 Qy 729 GAPVTVFLGNVMYFAFLFTVVLVDRPPPGQSPGPREVTLYFWVFTLVLEIRQGGFF 788
 Db 1139 SAPISFWSWTISFILFIPTTLLV--KTPPR-PTVIEYILIAVAAFGLSQVRKILM 1195
 Qy 789 TDETHLVKKFTLYVGNWNKMDMVAIFLIVGVTCRMLPSAFEAGRTVLAMDPMVFTLR 848
 Db 1196 SDAPK-FYEKIRTYVCSFNCVTLAIIFYIVGFMRFCGSV-AYGRVILACDSVLWTMK 1253
 Qy 849 LIHIFALHKQKPKLIIVVERMMKDVFFLFFLSVMLVAVGTVTQALLHHDHGRLEWIF-R 907
 Db 1254 LLDYMSVHPKLGYPVTMAGMIONMSYIIVMLVTLISFGLARQSTYP-DETMHWILVR 1312
 Qy 908 RVLYRPYLQIFGQIPLDEIDEARVNGSTH-----PLLEDSP---SCPSLYANWL 954
 Db 1313 NIFLKPYFMYLGEVYADEID---TCGDEAWDQHLNGGPFVILNGTTGLSCVPGY--WI 1366
 Qy 955 VILLVTFLLVTVNVLNMLLIAMFSYTFQVQGNADMFWKFORYNLIVYHERPALAPPF 1014
 Db 1367 PPLLMTFFLLIANILLMSMLIAIFNHIFDQTDMSQIWLQRYKQVMEYESTFPLPPPL 1426
 Qy 1015 ILLSHLSLTIRRVFKKEAEKHREH-----LEEDLPDLDQKVVTWETQKENFL-S 1064
 Db 1427 TPLHGVLLIQFVTRLSCKSQERNPILLKIAELFDNDQIEKLHDFEEDCMEDLARQ 1486
 Qy 1065 KMEKRRRDSGEVIRKTAHR-----VDFIARYKLG---LREQEKRIKCLSQINCSV 1114
 Db 1487 KLNKETSNEQIRLDIRDQILNKLIDLQAKESMGDRVINDVESRLASVEKAQN---E 1543
 Qy 1115 LVSSVADVLAQGGPRSSQHC 1135
 Db 1544 ILECVRALLQNNAPTAIGRC 1564

886 FYSSPTKFWSCIAFLIPLTWTQTCLLLE---TSLKPSKYEWITFTYTTVTLSEHIRK- 941
 787 PFTDEDTHLVKFTLYVDGNWKNCDMAIFLFLVGVTCRMLPSAFE-GRTVLAMDFWVF 845
 942 LMTSEGRINEKVKFYAKYNIWTSAALLFFLVGVGFRFLVPMYRHSWGRVLLSFSNVLF 1001
 846 TRLIHIFAHKQLGPKPIIVVERMMKDVFFFLPFLSVLVAVGYTTQALLHPHDGRLEWI 905
 1002 YMKIFEYLVHPILGPYIQMAAKWWSMCYICVLLVPLMAFGVNRQALTEPNVKDHWL 1061
 906 F-RRLVYRYPQLQIFGQIPDLDEIDEARVNCSTHPLLEDSPCSPLSYANWLVLILLVTFL 964
 1062 LVRNIFKPYFMYLGEVYAGEID---TCG-----DEGIRCFPGY--FIPPLLMVIFLL 1109
 965 VTNVLLMILLAMPSTYFQVQGNADMFKEFORNLVIVEYHERPALAPPFILLSHL----- 1020
 1110 VANILLNLNLTAIPNNIYNDISIEKSEIKWLFQRYQQIMVHDSFLLPPPSFIAHVTHFI 1169
 1021 --SILTRVRPKK-----EAEHKKR-EHLERDLPDPLDQKVVTWETVOKENFLS 1064
 1170 DYLNLRRPDTKPRSRSEHSIKLSVTEDEMKKIQDFEEDCIDTLTR-----IRK---L 1218
 1065 KMEKRRRDSGEVLKRTAHRV-----DFTAKYLGGLRBEOKRIKCLSEQINYSGLVSS 1118
 1219 KLNTKEPLSVTDLTTELTCQRVHDLMQENFLKK-----SRVYDIETKIDHISNSSDE 1266
 9119 VADV 1123
 1270 VQIL 1274

 RESULT 4
 T18951
 hypothetical protein C05C12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T18951
 R:White, S.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: Z19050
 A:Accession: T18951
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1707 <N>
 A:Cross-references: UNIPROT:Q17652; EMBL:Z68333; PIDN:CAA92726.1; GSPDB:GN00022
 A:Experimental source: clone C05C12
 C:Genetics:
 A:Gene: CESP:C05C12.3
 A:Map position: 4
 A:Introns: 13/3; 52/1; 82/3; 100/3; 174/3; 203/1; 249/2; 292/1; 358/2; 406/2; 454/2/3; 1595/1; 1647/2; 1673/3; 1695/3

 Query Match 14.6%; Score 889; DB 2; Length 1707;
 Best Local Similarity 22.3%; Pred. No. 8.2e-56;
 Matches 308; Conservative 229; Mismatches 456; Indels 390; Gaps 43

 26 GEVNPFGSGKRGKFRVPVSGVAPSVLPDLLAEWHLPAPNLVSLVGEQPFAMKSWLR 85
 197 GNIVFEGTA-HHAQYARISFSDPRDI VHLMMKWKLPKPKLIITINGGLTKFDLQPKLA 255

 86 DVLRKGLVKAQOSTCAWILTSALRYGLARHVQAVRDHSLASTSTKRVVAVGMAASLGRV 145
 256 RTFRKGIMKIAKSTDAWITSGLDGVVKKHDSALHDI--GNHTSKNHWVVALGISAWGL 313

 146 LHRRILEBAQDFPVHYHPEDDGGSCGPLCSLSDNLSHFILVBPFGPGKDGGLTELRLE 205
 314 KQRS--RFVGKDSVTYATVFNNT-RLKELNDNHSYFLPSDNGTVNRYGAEIIMRKRLE 370

 206 KHISQRAGYGGTGIEIPVLCLVNDPNTLERISRAVE--QAAPWILVGGSGGIADV 263
 371 AYLAQ-----GDKKESAIPLVCVVLGGGAFTIKWHDYVTTIPRIPVIVCDGSGRAADIL 425
 264 A-----ALVNPQHILV--PKVAEQKFEKFPKSHFSDWEDIVRWTKL 302

Db 426 APAHQVQSQNGFSLDNIRNQLNIVIRIFGYDPTKTAQKLKIQ----- 467
QY 303 LQWITSHQHLTVYDFEQSGSELDVTILKALVACKSHSQBPQDYLDLKLAVAMDVRD 362
Db 468 IVECSNKLMTIFRLGSSREDLHVIMSCLL---KQNLSP---EQQLALANRAD 521
QY 363 IAKSEIFNGDVWKSCLDEVMVDALVSNKPEFVFLFVDNGADVADFLTYGRLOELY--- 419
Db 522 IARTIFANGTWTQDLNAMIETALSNDRIDFVHLLLENGVSMQKFLTYGRLEHLNNTD 581
QY 420 ---RVSVKSLFDLLQKQBEARLTLAGLGTQQAEPGAPPAFAFHSVRLKDPLOD 476
Db 582 KGQONTLRNLVDSKHH-----IKUVEGRVLNVMGN 615
QY 477 ACRGPFYQD-----GRPDERRAEK----- 495
Db 616 LYKSNYTKPEFNQYVFNRRKQFGKRVHNSNGRNDVIGPSGDAGRERMSQSLIN 675
QY 496 -----GPAKPTGQKWLLDLNQKSEN-----PWRLFLMVLQNHWMATY 536
Db 676 NARNSIISLFGCGGKRESDEDDPSNLESEANNDFTFRYPYSDLMIAWLVITKQKMAKL 735
QY 537 FWAMQGEVAAALACKILKEMSHLETEAARATREA-----KYERLALDLFS 585
Db 736 MWTGSEGMALVASRL-----YVSLAKTASLATGEIGMSQDFTBFSDEFSSELAVEVLE 790
QY 586 EYGSNEARAFALVRNRCWSKTKLHLATEADAKAFPAHDGVOAFLTRIWWGDMA--- 642
Db 791 YCTKHGRDQTLRLTLCELANWGETCLSLAANGHRRKFLAHPCCMLLSDWQGLLMKN 850
QY 643 -AGTPIRLLAGAFCLPALVNTNLTSEAPLR-----TG 676
Db 851 NQNSKVLTCIAA---PPLIF--LLGFKTEQLMLQPKTAAEHDEMSDSEMSAEDTDS 905
QY 677 LEDLDLSDLTE-----KSPLYGLQSRVEELVEA 706
Db 906 SDSSSDSDDEDAKLRAQSLADQPLSIHLRLVRDKLNFSEKKKPDGMG--ISRIVVA 961
QY 707 P-----RAQ----- 710
Db 962 PPIVTRGNRARTMSIKKSKNVIKPPACLKLETSDDEQEQKATEMCKSTFFDFPDP 1021
QY 711 ---GDRGPRAV-----FLTR-----WRK 726
Db 1022 YINRTGKGSVAMHNDMDYDPSBELDTQTRQKSSREFSSRNVTYQVTRPLSMWK 1081
QY 727 ---FWGAPVTVLGNVMYFA---FLFLTYVLLVDFRPPPPQSGPGEVTLXFWVETLV 779
Db 1082 KIMEFYKAPITTYW---LWFFAFIWFLLITLNLVKTQ---RIASWSEWTVFAYIFWT 1135
QY 780 LE---BIRQGFTEDETHLVKFTLYVGDNNWKNCDMAIFLIVGVTCRMLPSAFAEAGRT 836
Db 1136 LEIGRKVSTIMMDTSKPVLKQLRVFFQYRNGLLAFGLLTLYLAYTIRLSPTKTLGRI 1195
QY 837 VLMDFMVFTRLIHIPAHKQLGPKIIVVERMKNDVFFFLFSLVMLVAVGVTTQALLH 896
Db 1196 LIICNSVMSLKVLYSLVQOGLGPGYINVAEMITPMLPLCVIYFITYAFGLRQITY 1255
QY 897 PHDGRLEW---IFRRVLVRYLQIFGQPLDEIDBARVNCSTHPLLEDSPSCPSLYAN- 952
Db 1256 PVE---DHWILVRNIFTQPFMYLGEVYAAEID---TCGDEIWTQTHEDENIPISMLNV 1308
QY 953 ---WLVLLVTLFLLVTLNVLNLLIAMFSYTFQV-VQGNADMWKEQRVNLIV 1002
Db 1309 THETCVPGYWIAPVGLTVFMLATNVLNVMVACVIFEKHQSTREIF-LFERVGGVM 1367
QY 1003 EYHERPALAPFILLSHLSLTLRVFKKEAHHKEHL-ERDL-----PDPLDQKVTWET 1056
Db 1368 EYESTWLPPTTIYHVIMFLKIKSSSRMRFKNLFDQSLKFLSPDEM-EKVHTPEE 1426
QY 1057 VOKENFLSKMRKRDRDSEGEVLRKTAHRVDVFIKYLGLL-----RQEKRIKCL 1105

Db 1427 ESVDKMKRETKNLSNDRIRHTAERTDAILNRVSHLTQLEFTLKEIRELSHKMKN 1486
QY 1106 ESQ 1108
Db 1487 DSR 1489
RESULT 5
JU0092
trp protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-Nov-2000
C:Accession: JU0092
R:Montell, C.; Rubin, G.M.
Neuron 2, 1313-1323, 1989
A:Title: Molecular characterization of the Drosophila trp locus: a putative integral mem
A:Reference number: JU0092; MUID:90180449; PMID:2516726
A:Accession: JU0092
A:Molecule type: mRNA
A:Residues: 1-1275 <MON>
A:Experimental source: strain Oregon R
C:Comment: trp protein is expressed predominantly in the rhabdomeric membranes of the ph
C:Genetics:
A:Gene: trp
A:Cross-references: FlyBase:FBgn0003861
C:Superfamily: TRPC3 protein
C:Keywords: transmembrane protein
F:334-354/Domain: transmembrane #status predicted <TM1>
F:378-401/Domain: transmembrane #status predicted <TM2>
F:419-436/Domain: transmembrane #status predicted <TM3>
F:457-471/Domain: transmembrane #status predicted <TM4>
F:504-527/Domain: transmembrane #status predicted <TM5>
F:612-630/Domain: transmembrane #status predicted <TM6>
F:636-661/Domain: transmembrane #status predicted <TM7>
Query Match 5.4%; Score 326.5; DB 2; Length 1275;
Best Local Similarity 20.3%; Pred. No. 4.8e-15;
Matches 178; Conservative 123; Mismatches 264; Indels 313; Gaps 37;
QY 305 NITSHQHLTVYDFEQSGSELDVTILKALVACKSHSQBPQDYLDLKLAVAMDVRDIA 364
Db 86 NVLLIEHNTVEGDALLHAISEYVEAVESELLQWETNKEGQPY-----SWEAVDRS 137
QY 365 KSEIFNGDVWKSCLDEVMVDALVSNKPEFVRLFVDNGA-----DV 406
Db 138 KS-TFTVDI-----TFLIAHRNNYELIKILLDRGATLPMPHDVKCCDCSVTSQT 188
QY 407 ADPLTYGRILQ-ELYRSVSKSLIPDLLQKQBEARLTLAGLGTQQAEPGAPPAFAFSLH- 464
Db 189 TDSLRSQSRLNAYBALSSLI-----ALSSRDPLV--TAFQLSW 227
QY 465 EYSRVLKDFLODACKGFGYQDGRPDGRRRAEKPAKRPYTGQKWLLDLNQKSENPRDILFW 524
Db 228 ELKRL--QAMESFEPAEYTEMR---QMVQDFGTS-----LLDHARTS-----MELE 268
QY 525 AVLQNRHEMATYFWAMGOEGVAAALACKILKEMSHLETEAARATREAKYERLALDLP 584
Db 269 VMLNPNHPSHDINCLGQ-----RQTLER----- 292
QY 585 SECTYSNEARAFALVRNRCWSKTKLHLATEADAKAFPAHDGVOAFLTRIWWGDMAAG 644
Db 293 -----LKLAIKYKQKTFVAHPNVQQLAAIIVYD---G 321
QY 645 TPILRLLAGFLCPALVNTNLTTFSEAPLATGLDQLDLSLDTKSPLYGLQSRVEELV 704
Db 322 LPGFR-----RKQASQQLMDVVVKGC-SFFIYSL-----KYI 352
QY 705 EAPRAQDGRGPRAVFLLTRWRKFWGAPVTVFLGNVVMYFAFLF----- 748
Db 353 LAPDSEG-----AKPMRKPFVKFIHSCSYMFFLMLGAASLRVVVQITFELL 399
QY 749 -FTYVL--LVDFRPPQ--PSGPEVTLVFWFVLVEIR-----QGFTDETHLVKKF 799

Db 400 APPMWTLMEDWRKHERGSLPGPIELAIITVIMALIFEELKSLYSDGLFE----- 449
Qy 800 TLYVGDVNNKCDMVAIFIVGVTCR-----MLPS 829
Db 450 --YIMDLNWIIVDYSNMFYVWILCRAYAWIVHRLMFRGIDPYFPRHHHPDPDMLLS 507
Qy 830 --APEAGRTVLAMDPMVFT-LRLIHPAIHQKLGPKIIVVERMMKDVFFFLFSLVWLVA 886
Db 508 EGAFNAG-----MVFSYKLVHIFSPHPLGLOVSLGRMIIDIIKFFFIYTLVLF 559
Qy 887 YGVTTQALL-----HPHDGRLEW-----IFRRV--LYRP-----YLIQIFGQ 920
Db 560 FCGGLNQLLWYVAELEKNCYHLHPDVADFDQEKACTIWRFSNLFETSSQSLFWASFL 619
Qy 921 IPLDEIDARVNCSTHPLLEDSPSCPSLYANWLIVLLVTLVTLVTLVTLVTLVTLV 980
Db 620 VDLVSFIDLAKIS-----FTRFWALLMFGSYVINIIVLLNMLIAMNSN 663
Qy 981 TFOVVGQNMADMPKFORYNLIVEYHE-RPALAPPFILLSHLSLTLRRVFKKEAEHREHL 1039
Db 664 SYQIISERADTBKFAWSQSLMSYFEDGGTIPPPNLCPNMKMLKTLGRKPSRTKSM 723
Qy 1040 ERDL--PDPLOKVVVTWQKFNFLSKMEKRRDSEG 1075
Db 724 RKSMEQAOTLHDKVM---KLLVRYIT-AEQRRDDYG 757

RESULT 6
JN0015
trp protein - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001
C:Accession: JN0015
R:Wong, F.; Schaefer, B.L.; Roop, B.C.; LaMendola, J.N.; Johnson-Seaton, D.; Shao, D.
Neuron 3, 81-94, 1989
A:Title: Proper function of the *Drosophila trp* gene product during pupal development is
F:191,602,880,883,924/Binding site: phosphate (Ser) (covalent) #status predicted
F:800,1266/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 5.2%; Score 317.5; DB 2; Length 1274;
Best Local Similarity 20.3%; Pred. No. 2,2e-14;
Matches 187; Conservative 132; Mismatches 273; Indels 327; Gaps 41;

Qy 274 VPVAKK-QPEKFPKSHSWEDIVRWTKLQNTSH-----QHLLTVDFDQEGS 323
Db 48 VKKILEYQGTDFK---NINCTDPMNRSALISAIENENFDLMVILLHEINIEVDALLHAI 104
Qy 324 EELDTVLKALVACKSHSQEPQDYLDELKLVAMORVDIAKSEIFNGDVEWMSCDLEEV 383
Db 105 SEBYEVAEVELLQWEETHNKEGOPY-----SWEADVRSKS-TFTVDITF----- 147
Qy 384 MVDALVSNKEFVRLFDVNGA-----DVADFLTVGLRQ-ELYRSVSR 424
Db 148 LILAAHNNYIILKILLDRATLPMPHDVKCGDCVTSQTDSLRSQSRINAYRALSA 207
Qy 425 KSLFLDLLQKQBEARLTLAGLQQAQREPPAGPAPSLH-EVSRVLKDFLOQACRGFYQ 483
Db 208 SSLI-----ALSRDPLV--TAPQLSWELKRL--QAMESEFAEY 244
Qy 484 DGRPGDRRAEKGPAKPTQCKQLLDLNQKSENPWRDLFLWAVLQNHENATYFWAQGE 543

Db 245 EMR---QMVODFGTS-----LLDHARTS-----MELEVMLNFNHPSHDIW----- 282
Qy 544 GVAALAAACKILKEMSHLETEAEARATREAKYERLALDLFSECVSYNSEARAFALLVVRN 603
Db 283 -----CLASSET-----LER-- 292
Qy 604 RCWSKTTLHLATADAKAFPAHDGVQAFALFRIWGDMAAGTPIRLLLGAFCLCPALVTN 663
Db 293 -----LKLAIRYKQKTFVAHPNVQOLLAIIW-----YDG 321
Qy 664 LITSEERAPLTGLDLODLSLTERKSPYGLQSRVEELVEAPRAQDGRGRAVFLLTR 723
Db 322 LPGPPOEAS-----QQLMDVVVKLG-C-SPIIYSL-----KYLAPUSEG----- 358
Qy 724 WRKFGWAPVTFLGNVVMYFAPFL-----FTYVL--LVDFRPPPOG-- 763
Db 359 -AKWRNPLSSSRTPCSYMFLLMLLGRASLRVQVITFELLAFPMWLTLEDWRKHERGS 417
Qy 764 -PSGPEVTLYFWFTLVLEIR-----QGFDTDEDHLVKFTLYVGDNNKCDMVAIFL 818
Db 418 LPGPTELAIITVIMALIFEELKSLYSDGLFE-----YIMDLNWIIVDYSNMF 465
Qy 819 IVGVTCR-----MLPS--APEAGRTVLAMDPMVFT 846
Db 466 VTWILCRATAWIVHRLMFRGIDPYFPRHHHPDPMLLSEGAFAG-----MVFS 517
Qy 847 -LRLIHPAIHQKLGPKIIVVERMMKDVFFFLFSLVWLVAIXGVTTQALL----- 895
Db 518 YLKLWHIIFSIHPHGLQVSLGRMIIDIIKFFFIYTLVLFAGCGLNQLLWYVAELEKNC 577
Qy 896 --HPHDGRLEW-----IFRRV--LYRP-----YLIQIFGQIPLDEIDARVNCSTHPL 939
Db 578 CYHLHPDVADPDQEKACTIWRFSNLFETSSQSLFWASFLVDFSLVDFLAGIKS----- 631
Qy 940 LEDSPSCPSLYANWLIVLLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLV 999
Db 632 -----FTRFWALLMFGSYVINIIVLLNMLIAMNSYQIISERADTBKFAWSQ 681
Qy 1000 LIVEYHE-RPALAPPFILLSHLSLTLRRVFKKEAEHREHLERDL--PDPLOKVVVTW 1056
Db 682 LMWSYFEDGGTIPPPNLCPNMKMLKTLGRKPSRTKSMRKSMEQAOTLHDKVM---K 738
Qy 1057 VQKENFLSKMEKRRDSEG 1075
Db 739 LLVRYIT-AEQRRDDYG 756

RESULT 7
S40764
hypothetical protein ZK512.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: S40764
R:Hawkins, T.; Ainscough, R.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40759
A:Accession: S40764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1418 <HAW>
A:Cross-references: UNIPROT:P34641; EMBL:Z22177; NID:g297989; PID:g297992
C:Genetics: 199/1, 238/1, 290/2, 529/3, 557/3, 588/3, 677/2, 733/3, 772/3, 846/3, 946/1;
A:introns: 199/1, 238/1, 290/2, 529/3, 557/3, 588/3, 677/2, 733/3, 772/3, 846/3, 946/1;
C:Superfamily: *Caenorhabditis elegans* hypothetical protein ZK512.3

Query Match 4.8%; Score 294; DB 2; Length 1418;
Best Local Similarity 20.2%; Pred. No. 1.3e-12;
Matches 222; Conservative 174; Mismatches 437; Indels 264; Gaps 45;

Qy 65 PNLVSLVGEQEPFANKSWLRDVLRLGLVKAAQSTGAWILTSALRVGLRHVQAVRDHS 124
Db 67 POLIISLISHGNSLSTK--YMSSVENGLKSLFGCGTWLISSG-----EYNDPM 113

Db 430 LELIVVMYVIGFVWEVEQIEFAVGMS-----YLRNMWNFIDFLRNSLY-VSVMC-L 479
Qy 827 LPSAFAGRTVLAM-----FMVET-LRLIHFIAHKQL 859
Db 480 RAFAYIOQATARDPOMAYIPREKWHDFDPLIAEGLFAAANVPSALKVHLFSINPHL 539
Qy 860 GPKIIVVERMMKDV--FFFLPFLSVLVVAYGV-----TQALLHHDGRLEW-- 904
Db 540 GPLQISLGRMWDIVKFFPIYTLVLFACGLNQLLWYFAALEKSKCVLP-GGEADWGS 598
Qy 905 -----IPRV--LVPR-----YLQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYAN 952
Db 599 HGDCMKWRFRGNLFESSQSFLWASFGVMGLDDFELSGIKS-----YTR 642
Qy 953 WLVLILLVTFLLVTVLLVLLIIMFSTYFQVQGNADMFWKFORYNLIVEYHERPA-LA 1011
Db 643 FGLMLFGSYVINIVILLNLLIAMSNYSAMIDEHSDEWKFAPTKLWMSYFEDSATLP 702
Qy 1012 PPFILLSHLSLTLRRVFKAEHREHLERDLPDQKVVTVETVQKENFSLKMKERRR 1071
Db 703 PPFNVLPVKWVI-RIFKSS-----KTIQRQSKRKEQBOF 739
Qy 1072 DSEGEVLKTAHRVDVFIKYLGLREQ-----EKRIKLESQIN 1110
Db 740 SEYDNIMR-----SLVWRYVAAMHRKPPNNPVSEDDINEVKSEIN 779

RESULT 9
F88391
protein R06B10.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: F88391
R:Anonymous, The C. elegans Sequencing Consortium.
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see websites genome.wustli.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: F88391
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-899 <STO>
A:Cross-references: GB:chr_III; PIDN:AA895033.1; PID:G2746879; GSPDB:GN00021; CESP:R06B1
A:Gene: R06B10.4
A:Map position: 3

Query Match 4.1%; Score 247; DB 2; Length 899;
Best Local Similarity 19.4%; Pred. No. 1.7e-09;
Matches 166; Conservative 125; Mismatches 312; Indels 252; Gaps 38;

Qy 349 LDELKLAVDNRVDIAKSEIFNGDVEWKSDDL-----EYVMDALVSNKPEFVRLFDV 401
Db 32 LREKQPLLCERCDIGSVRKLAGISTEFTNCLDPLGRNALLIAENIEMIELLD 91
Qy 402 NGADVADFTYQRLQELYSVSKSLLDLQKQKQ-EARLTAGLGTQQAEPAGPPA 460
Db 92 HNITGDAIYALGEE--NVEAVEIIVHELEKMDKFDSEKQGVETESAPTDITP 148
Qy 461 FSLHEVSRVLKDFLOACRGFYODGPRDRRAEKGPAPKPP-----TGQKWL 508
Db 149 LAAH-----KONYE--CIKFLD-----KKGTVPHPHDVRCSPCEYVARBEDSL 191
Qy 509 DLNOKSENPRDLFLWAVL--ONRHEMATYFWAQGVAAALAAACKILKEMSHLETEAEA 567
Db 192 RLRSRINAVRALTSPSLICLSARDPILYAFELSW-----LKELSFIEFPRT 240
Qy 568 ARATREAKYERLALDLFSECYSNSEARAFALLVRNRCWSKTTTC-----LHLAT 616
Db 241 DYEELSQCKQKFCVHMLDQVRGSKLEL--VVLNHTTNAMHDVTSANYGNPEKLARKLAI 298
Qy 617 EADAKAFFAGHDGVOAFLTRIWGDMAAGTPIRLGLGFLCPALVYTNLITFSEAPLRTG 676

Db 299 QLSQKRFVAHPNCQQLLDIWI-----EGVESVR-----CTNFIY-KLIFY----- 338
Qy 677 LEDQLDLSLDTEKSPLYGLSQSRVEELVEAPRAQCDRGPRAVFLL-----TRWRKFWGADVT 733
Db 339 -----ILQMLGFLPLFSL-----VYLLAPHSSMGQFAKKDFI 369
Qy 734 VFLGNVMYFAFLFITY-----VLVD-----FRPPQGPSGPEVTLYFWVFT 777
Db 370 KFLSHSGSYIFFLLIMASQRMVNIDILRTDDVDKRETRGPP--PTIIECAIFLWVLG 427
Qy 778 LVLSEIRO-----GFTBEDTHLVKFTLYVGDNNKCDMVAIFLFIIVGTCTCML----- 827
Db 428 LIWVEIKQLWECGLYN-----YCRNLWNILDFITNSLYLTALRVVAVIQVE 475
Qy 828 PSFAEAGR-----TVLAMDFM-----VF-LRLIHFIAHKQLGP-KII 864
Db 476 QEALRANSVHTARHLPRRDWDAMPDILLSECFATANIFSSILKLVHITVSPHLGLKIS 535
Qy 865 VVE-----RMMKDV--PFFFLSVLVVAYGVTTQALLPHDGRLEWIFRRV- 909
Db 536 LGELEKFWKKTLCRMVIDIVKFFMVYALVLFAPACGL-----NOLLWYASMR 585
Qy 910 -----LYRPY-----LQIFGQIPLDEIDARVNC-----THPLL 940
Db 586 QNECNLYEQYKNEKSLSYKYEHLKESCDCKYKSCSIYHTAETLFWALFGLVDLTHFLK 645
Qy 941 EDSPCPSLYANLVILLVTLVTVLLVLLIIMFSTYFQVQGNADMFWKFORYNL 1000
Db 646 ED-----HFLSEWGTGTIFGSCCSIIVLNMLIAMNSYQYISDQADIEWKARSRL 700
Qy 1001 IVEYHERPA-LAPPFILL---SHLSLTLRRVFKAEHREHLERDLPDQKVVTVWET 1056
Db 701 FLEYEDDTATPPPPNIVPSPKSIYVCHLYTLKLCNCTK-----LQPSKOKSM---R 751
Qy 1057 VOKENFLSKMKRRR 1071
Db 752 VESKNLAIRQRPKQ 766

RESULT 10
S44873
ZC21.2 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C:Accession: S44873
R:Du, Z.; Waterston, R.
A:Description: Sequence of the C. elegans cosmid ZC21.
A:Reference number: S44649
A:Accession: S44873
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-823 <DUZ>
A:Cross-references: EMBL:L16685; NID:G289729; PIDN:AAA28168.1; PID:G289732
C:Genetics:
A:Introns: 47/2; 91/3; 144/1; 215/2; 344/3; 394/3; 440/3; 506/2; 566/3; 756/3
C:Superfamily: TRPC3 protein
C:Keywords: transmembrane protein

Query Match 3.9%; Score 235.5; DB 2; Length 823;
Best Local Similarity 20.7%; Pred. No. 1e-08;
Matches 113; Conservative 92; Mismatches 190; Indels 151; Gaps 20;

Qy 549 LAACKILKEMSHLETEAARAT---REAKYERLALDLFSECYSNSEARAFALLVRNR- 604
Db 260 LSAFLKSWDLQRLAFEEHEFKETYLQLSQCKQYSCDLLSQCRSEE--VIAILNKGDNV 317
Qy 605 -----CWS---KTTCLHLATEADAKAFHAGDVGQAFLTRIWGDMAAGTPIRLGLA-- 653
Db 318 NDDNIDVWASKLSLSRLKLAIKYEQKAFVSHPHCQQLTSITWY-----EGIPYQRSGTWA 373
Qy 654 --FLCPALVYTNLITFSEAPLRTGLDQLDLSLDTSEKSPLYGL-----QSRVEELVE 705

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Db      374 NFELYAFLLFL-----WPIFCLMYILMPKSLRGLRVR 405
QY      706 APRAQGRGRPRAVELLTRWRKFGAPVTVFLGNVVMYFAFLFTYVLLVDP----- 757
Db      406 SP-----FMKFPYYSVS-----PATFGLLTWATFEDYRYEKGEG 441
QY      758 ---RPPPGQSGP--EVTLYFWVFTLVLEIEIQGFPTDTHLVKKFTLYVGDNNKCDM 812
Db      442 GMTRASDRGPATWVESLFTWVIGMLWSEIKQLW-----BEGFKRYMRQWNNWLD 493
QY      813 VAIFLPIVGTCTMLPSAFE-----AGRTVLAMDPMVFTLR 848
Db      494 LMICLYLCTISRL--SAYIITYREDPVRYTVRYTWTSEPMVLVASALFAGNVFSFAR 551
QY      849 LIHIFAIHKQLGPKLIIVVERMKDVFVFLFSLVNLVAYGVTTOALLPHDGRLEWIFRR 908
Db      552 IYLFQTNPYLGLQLISLGCMLVDVAKFCFVLIISFSISGLAQLWYDPTDVCPLG 611
QY      909 VLYRPLYQIFGQIPLDEIDEARVNGSTHPLL-----EDSPSPCS--LYANWLIVILL 958
Db      612 ATCKHSSNVFSSI-----ADSVLTLLWSLFSITKPEDTVVVENHKITQWVGQGM 660
QY      959 LVTFLLVTVNLLMILLIAMPYTFQVQGNAMFWKQRYNL-IVEYHERPALAPPE-II 1016
Db      661 FIMYHCTSIIVLLANMLIAMMHSFQIINDHADLEWKFRTKLMAHEDGSSLPFPFNII 720
QY      1017 LSHLSL 1022
Db      721 VTPKSL 726

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RESULT 11

JC5807

trp3 protein - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999

C/Accession: JC5807

R/Preutz, K.D.; Noeller, J.K.; Krause, E.; Gobel, A.; Schulz, I.

Biochem. Biophys. Res. Commun. 240, 167-172, 1997

A/Title: Expression and characterization of a trp1 homolog from rat.

A/Reference number: JC5807; MUID:98042538; PMID:9367904

A/Accession: JC5807

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Experimental source: brain

C/Comment: This protein participates in store-operated Ca2+ entry into cells.

C/Superfamily: TRPC3 protein

Query Match 3.2%; Score 192; DB 2; Length 828;
Best Local Similarity 19.8%; Pred. No. 1.5e-05;
Matches 154; Conservative 122; Mismatches 290; Indels 210; Gaps 31;

```

QY      381 EEWVDALVSNKDFVRLFPVDN---GADVADFLTYGLRQLYRSVRSKSL-LPDLILQK 435
Db      40 ERFDLAAEYGNIPVVRKMLEESRTLVNVCYDYNQALQ---LAVGNEHLEVTELLKK 96
QY      436 QBEARLTLAGL-----GTQAREPPAGPAFSLHEVSRVLKDFLODACRGFYQGRPGDR 490
Db      97 ENLARIGDALLAISGVYRIVEAILSHPALAQQTLSPLS-LRD--DDFYD----- 146
QY      491 RRAEGPAKRYT-----GQKW---LIDLNQSSENPWRDLFLWAVLQNHMAT-- 535
Db      147 ---EDGTRFSPDITPILAAHCHKYEVVHLLKGRTERPHDYLCRCADCAEQRLWTFPS 203
QY      536 -----YFWMQEGVAAALAAACKILKEMSHLETEAEARATREAKYERLA 580
Db      204 HSRSRINAYKASFCYLSLSEDPVLTALELSNELAKLANIEKEFNDRYKLSMQCKDFV 263
QY      581 LDLPSECVSNEARA-----FALLVRNRCSKTTCLHLATEADAKAFHAGDGVQAFLTR 635
Db      264 VGVLDLRCRDESEVAILNGDLESVEERHGHKASLSRVLKAIKYEKVFAPNCQQLIT- 322

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QY      636 IWMDMAAGTPIRLILGAPLCPALVYTNLITFSEAPLRTGLEDLQDLSLDTSKSPLYG 695
Db      323 IWGNLSGRGRIAIKCL-VVLVVALPFLAIGYWIAPC----- 359
QY      696 LOSRVEELVEAPRAQGRGRPRAVELLTRWRKFGAPVTVFLGNVVM---YFAFLFLFTY 751
Db      360 --SRIGKILRSP-----FMKFAVASFIIFGLLVFNASDRFEGCITTLPN 401
QY      752 VLLVD-----FRPPPGQSGPEVTLYFWVFTLVLEIEIQGFPTDTHLVKKFTLYVGDN 806
Db      402 ITVIDYPQKIFRVKVTQFTWTEMLIMVVLGMWSECKELWLEGPREYIVQL----- 453
QY      807 WNKCDMAVFIPIVGVTCRML----- 827
Db      454 WNVLDLFLSI--FIAAFTARFLAFLQATKAQYVDSHVQESDLEVTLPPEVQYFTYARDKW 511
QY      828 ---PSAPEAGRTVLAMDPMVFTLRHIFAIHKQLGPKLIIVVERMKDVF--PFLPFLSV 882
Db      512 LPSPDQIISGLYAIIV--VLSPRIATILPANESFGPLQISLGRITVKDIFKPMWLFIW 569
QY      883 WL-----VAYGVTTOALLPHDGRLEWIFRRVLYRPLYQIFGQIPLDEIDEARVNCST 935
Db      570 FLAFMIGMFIYSYLGAKVDPAFTTVBSFKTLFW---SIFG---LSEV-----T 614
QY      936 HPLLEDSPSCPS-----LYANWLIVLLVTFLLVTVNLLMILLIAMPYTFQVQGNADM 991
Db      615 SVVLKYDHKEFIENIGVLYGIYVNTWV-----VLLNMLIAMINSYQIEEDSDV 665
QY      992 FWKQRYNLIVEYHERPALAPPEIL---LSHLSLTLRRV-FKKEAEHKEHLEERDL 1043
Db      666 EWKPARSKLWSYFDDGKTLPPPLVPCPSFYVFMIRVNFPK---CRRRLQKDI 718

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RESULT 12

S68238

trp-1 protein - human

C/Species: Homo sapiens (man)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S68238

R/Zhu, X.; Chu, P.B.; Peyton, M.; Birnbaumer, L.

FEBs Lett. 373, 193-198, 1995

A/Title: Molecular cloning of a widely expressed human homologue for the Drosophila trp

A/Reference number: S68238; MUID:96033971; PMID:7589464

A/Accession: S68238

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-793 <ZHU>

A/Cross-references: UNIPROT:P48995; EMBL:U01110; NID:g1072042; PIDN:AAA93251.1; PID:g107

C/Superfamily: TRPC3 protein

C/Keywords: alternative splicing

Query Match 2.9%; Score 176.5; DB 2; Length 793;
Best Local Similarity 18.1%; Pred. No. 0.0002;
Matches 116; Conservative 106; Mismatches 215; Indels 203; Gaps 27;

```

QY      555 LKNSHLTE-----AEARATREAKYERLALDLFSECYSNSEARAF----- 596
Db      244 LKELSLVEFRNDYSELAR-----QCKMFAKOLLAQARNRELEVLNHTSDEPLDKR 298
QY      597 ALLVRNRCSKTTCLHLATEADAKAFHAGDGVQAFLTRIWMGDMAA--GTPILRLLAGF 654
Db      299 GLLEER-----MNLRLKLAIKYKQKEFVSQSQCOQFLNTVWFQMSGYRKRKTCCKIMTV 354
QY      655 LCPALVVTNLTITSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQGRG 714
Db      355 LTVGIFW-----PVLISLCYLI-----APKSO----- 375
QY      715 PRAVFLTLTRWRKFGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPGQSPG-----EV 769
Db      376 -----FGRIHTFPFKMFIHIGASYSFTFLLLLNLISLV-YNEDKNTMTGPALERIDY 425
QY      770 TLYFWVFTLVLEIEIQGFPTD-EDTHLVKKFTLYVGDNNKCDMAVFIPIVGVTCRMLP 828

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Db 426 LLLILMIGWSDIKRLWYEGLED-----FLEESRNQSLFVWNSLYLATFALKVVA 476
 QY 829 -----SAFEAGRTVLAMDPMVFT-----LRLIHFAIHKOLGPKIIVVERMM 870
 Db 477 HNKPHDFADRKWDAPHP--TLVAEGLFAPANVLSYLRFFMYTSSILGLQIISMGQML 534
 QY 871 KDV--FFFLFELSVMLVAYGVTTQALLPHDGRLEWIFRRLVYRPYLQIF--GOIPLDEI 926
 Db 535 QDFGFLGFLVLSFTIGLT-----QLYDKGYTSKEQK 569
 QY 927 D-----EARVNCSTHPLLEDSPSCPSLIYANWLVI-----956
 Db 570 DCGVIFCEQSQSNDTHPSFI---GTCFALF--WYIFSLAHVAIFVTRFSYGBELQSFVGA 623
 QY 957 LLLVFLVTVNLLVLLMLLIAMSYTFQVVOGNADMFQRYNLIYEV-HERPALAPPE- 1014
 Db 624 VIVGTYNVVVVLTKLLVAMLHKSFQLIANHEDKEWKFARAKLWLSYFDDKCTLPPPPFN 683
 QY 1015 -----ILLSHLSLTLLRRVFKAEHKEHLE--RDLPOPLDQKVVTWETVQK---- 1059
 Db 684 IIPSPKTCYMISSLSKWCISHTSGKVRQNSLKEWRNLKQKRD-----ENYQKVMCC 737
 QY 1060 --ENFLSKMEKRRDSEGEVLRAKTAHRVDFIAKYLGGLRE 1097
 Db 738 LVHRYLTSMRQKQSTDOATVENLNLRODLSKFRNEIRD 777

RESULT 13

TRPC1 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
 C:Accession: I38361
 R:Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.
 Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
 A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.
 A:Reference number: I38361; MUID:96003837; PMID:7568191
 A:Accession: I38361
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-810 <RES>
 A:Cross-references: EMBL:X89056; NID:g1019786; PID:g1019787
 C:Superfamily: TRPC3 protein

Query Match 2.9%; Score 176.5; DB 2; Length 810;
 Best Local Similarity 18.1%; Pred. No. 0.0002;
 Matches 116; Conservative 106; Mismatches 215; Indels 203; Gaps 27;
 QY 555 LKEMSHLETE-----AQAARATREAKYERLALDLFSECYSNSARAF-----596
 Db 261 LKELSLVEFRNDYEELAR-----QCKMFAKOLLAQARNSRELEVILNHTSSDEPLDKR 315
 QY 597 ALLVRRNRCSKTTCLHLAEADAKAFPAHDGVAFLRIWVGDMAA--GTPILRLIGAF 654
 Db 316 GLLEER-----WNLRLKLAIKYQKEFVSQNSCOPLNTWFGOMSGYRKPKCKKIMTV 371
 QY 655 LCPALVYTNLITFSEEAPLRTGLEDLQDLSLDEKPSPLYGLQSRVEELVEAPRAQDGR 714
 Db 372 LTVGIFW-----PVLSLCYLI-----APKSQ-----392
 QY 715 PRAVFLTLRWRKFWGAPVTVPLGNVVMYFAFLFTVTVLLVDVFPVPPQSGP-----EV 769
 Db 393 -----FGRIIHTPFMKFIHICASYFTFLLLNLNLSLV-YNEDKKNWGPALERIDY 442
 QY 770 TLYFWVTVLLEERQGFDT-EDTHLVKFTLVVGNWNNKCDMVAIFLVGTCTRMPL 828
 Db 443 LLLIWIIGMISDILKRLWYEGLED-----FLEESRNQSLFVWNSLYLATFALKVVA 493
 QY 829 -----SAFEAGRTVLAMDPMVFT-----LRLIHFAIHKOLGPKIIVVERMM 870
 Db 494 HNKPHDFADRKWDAPHP--TLVAEGLFAPANVLSYLRFPMTTSSILGLQIISMGQML 551

QY 871 KDV--FFFLFELSVMLVAYGVTTQALLPHDGRLEWIFRRLVYRPYLQIF--GOIPLDEI 926
 Db 552 QDFGFLGFLVLSFTIGLT-----QLYDKGYTSKEQK 586
 QY 927 D-----EARVNCSTHPLLEDSPSCPSLIYANWLVI-----956
 Db 587 DCGVIFCEQSQSNDTHPSFI---GTCFALF--WYIFSLAHVAIFVTRFSYGBELQSFVGA 640
 QY 957 LLLVFLVTVNLLVLLMLLIAMSYTFQVVOGNADMFQRYNLIYEV-HERPALAPPE- 1014
 Db 641 VIVGTYNVVVVLTKLLVAMLHKSFQLIANHEDKEWKFARAKLWLSYFDDKCTLPPPPFN 700
 QY 1015 -----ILLSHLSLTLLRRVFKAEHKEHLE--RDLPOPLDQKVVTWETVQK---- 1059
 Db 701 IIPSPKTCYMISSLSKWCISHTSGKVRQNSLKEWRNLKQKRD-----ENYQKVMCC 754
 QY 1060 --ENFLSKMEKRRDSEGEVLRAKTAHRVDFIAKYLGGLRE 1097
 Db 755 LVHRYLTSMRQKQSTDOATVENLNLRODLSKFRNEIRD 794

RESULT 14

T34472
 hypothetical protein W03B1.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T34472
 R:Miller, N.; Bradshaw, H.; Wu, X.; Gattung, S.
 submitted to the EMBL Data Library, June 1998
 A:Description: The sequence of C. elegans cosmid W03B1.
 A:Reference number: Z21532
 A:Accession: T34472
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-823 <MIL>
 A:Cross-references: UNIPROT:Q23141; EMBL:U58753; PIDN:AAC24437.1; GSPDB:GN00022; CESP:W03B1
 A:Experimental source: Strain Bristol N2; clone W03B1
 C:Genetics:
 A:Map position: 4
 A:Introns: 70/3; 102/1; 137/2; 187/2; 265/3; 293/3; 357/3; 489/3; 516/1; 604/2; 628/2

Query Match 2.7%; Score 165; DB 2; Length 823;
 Best Local Similarity 22.9%; Pred. No. 0.0014;
 Matches 104; Conservative 64; Mismatches 175; Indels 112; Gaps 21;
 QY 771 LIPFWTVL-----LEEIRQ---GFTDETHLVKFTLVVGNWNNKCDMVAIFLFIQV 822
 Db 406 LAFWRIVLVVPLTLEAARLLIFAFVIEKKSSDKNF-----WSGA-----WVLIPI 452
 QY 823 TCMLPSAFEAGRTVLAMDPMVFTLRLIHFAIHKOLGPKIIVVERMMKDV-FFFFLFLS 881
 Db 453 TLELLCALPAIAT-----VSTLFFHSI---QSLGFFIHLFKKMMKTVGMFIIFCT 502
 QY 882 VWLVAYGVTTQALLPHDGRLE-----EWIFRRVLYRPIQIFQOIPLDEIDEARV--N 932
 Db 503 FWFVL-----AVIHVSISRTLLATNSFLYTVTFQKPEIFGEVQ---DEDIGILLN 552
 QY 933 CSTHPLLED-----SPSCPSLIYANWLIVLLVTVNLLVLLMLLIAMSYTFQV 985
 Db 553 CSEYNTKWEFDMYEAESCL--LFRSTIMPVFTYIFVTGILLVLLTAQTKEYENE 610
 QY 986 QGNADMFQRYNLIYEVHERPALAPPFILL-----1017
 Db 611 SKNSAYKGLYKTEQTKIESKLYLPFPFSLFVVLRFWYSCPKYIVITFTWLTSCCK 670
 QY 1018 ---SHLSLTLLRRVFKAEHKEHLELDLPDQKVVTWETVQENFLSKME-----K 1068
 Db 671 CSSTAISLWYRNIIVIVEGYPNGVARGTQDNEIDTKVAEFLRKRPDVALEKLDLVNNYD 730
 QY 1069 RRDSEGEVLRAKTAHRV-DFIAKYLGGLREQEKIKLESQINVCYSLVSSVADVLAQGG 1127
 Db 731 KDVDDE-EALKGLGKEIKKFLAKEIG--EBEREAQNSLENHPRSGSVLDPKKGHLS--- 784

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 18:08:14 ; Search time 192 Seconds
(without alignments)
3107.147 Million cell updates/sec

Title: US-09-834-792D-4
Perfect score: 6093
Sequence: 1 MQDVQPRPGSGDAEDRR.....HRGGLDGWEPGAGQPPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:
1: uniprot_prot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6093	100.0	1165	Q9NZQ8	Q9NZQ8 homo sapien
2	6039	99.1	1159	Q9NY34	Q9NY34 homo sapien
3	5088.5	83.5	1158	Q9JUN7	Q9JUN7 mus musculus
4	5036.5	82.7	1148	Q9EPM4	Q9EPM4 mus musculus
5	5026.5	82.5	1148	Q9NMF9	Q9NMF9 mus musculus
6	4981.5	81.8	1116	Q9EPM3	Q9EPM3 mus musculus
7	4465.5	73.3	1030	Q8BS44	Q8BS44 m mus muscu
8	4354.5	71.5	1000	Q7TFL4	Q7TFL4 mus musculus
9	2448.5	40.2	1214	Q8TD43	Q8TD43 homo sapien
10	2399.5	39.4	1213	Q7TN37	Q7TN37 mus musculus
11	2184.5	35.9	1040	Q96L84	Q96L84 homo sapien
12	2164	35.5	1016	Q9NXV1	Q9NXV1 homo sapien
13	2098	34.4	1069	Q7ZSD9	Q7ZSD9 homo sapien
14	2069	34.0	945	Q8BLM7	Q8BLM7 mus musculus
15	2039	33.5	1503	1 TRL2 HUMAN	Q94759 homo sapien
16	2021	33.2	1507	Q91YD4	Q91YD4 mus musculus
17	1924.5	31.6	872	Q6PDM0	Q6PDM0 mus musculus
18	1722	28.3	793	Q80Y94	Q80Y94 mus musculus
19	1582	26.0	1104	Q8RAD5	Q8RAD5 mus musculus
20	1579.5	25.9	779	Q7TOW9	Q7TOW9 xenopus lae
21	1567.5	25.7	1104	Q8RA55	Q8RA55 rattus norv
22	1565.5	25.7	1104	Q7Z2W7	Q7Z2W7 homo sapien
23	1563.5	25.7	1095	Q8TDX8	Q8TDX8 homo sapien
24	1563.5	25.7	1104	Q8TAC3	Q8TAC3 homo sapien
25	1334.5	21.9	1718	Q69ZB8	Q69ZB8 mus musculus
26	1312.5	21.7	1325	Q8EUL0	Q8EUL0 homo sapien
27	1312.5	21.5	1566	Q86WK3	Q86WK3 homo sapien
28	1307.5	21.5	1544	Q86WK2	Q86WK2 homo sapien
29	1307.5	21.5	1544	Q86Z00	Q86Z00 homo sapien
30	1307.5	21.5	1554	Q86SH6	Q86SH6 homo sapien
31	1303.5	21.4	1556	Q86WK1	Q86WK1 homo sapien

32	1303.5	21.4	1566	2	Q86WK4	Q86WK4 homo sapien
33	1300	21.3	1569	2	Q86Z01	Q86Z01 homo sapien
34	1300	21.3	1579	2	Q86SH0	Q86SH0 homo sapien
35	1286.5	21.1	846	2	Q6J3P5	Q6J3P5 homo sapien
36	1251.5	20.5	1526	2	Q86Y29	Q86Y29 homo sapien
37	1242.5	20.4	1527	2	Q7Z4N1	Q7Z4N1 homo sapien
38	1240.5	20.4	1533	2	Q75560	Q75560 homo sapien
39	1240.5	20.4	1533	2	Q7Z4N2	Q7Z4N2 homo sapien
40	1240.5	20.4	1533	2	Q7Z4N5	Q7Z4N5 homo sapien
41	1239.5	20.3	1533	2	Q7Z4N4	Q7Z4N4 homo sapien
42	1225	20.1	1070	2	Q7PT99	Q7PT99 anopheles g
43	1214.5	19.9	1862	2	Q925B2	Q925B2 mus musculu
44	1214.5	19.9	1863	2	Q923J1	Q923J1 mus musculu
45	1214.5	19.9	1863	2	Q9JLQ1	Q9JLQ1 mus musculu

ALIGNMENTS

RESULT 1

Q9NZQ8	Q9NZQ8	PRELIMINARY;	PRT; 1165 AA.
AC	Q9NZQ8		
DT	01-OCT-2000 (Tremblrel..15, Created)		
DT	01-OCT-2000 (Tremblrel..15, Last sequence update)		
DT	01-MAR-2004 (Tremblrel..26, Last annotation update)		
DE	MTR1		
GN	Name=MTR1;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20076317; PubMed=10607831; DOI=10.1093/hmg/9.2.2.203;		
RA	Pravitt D., Enklaar T., Klemm G., Gaertner B., Spangenberg C.,		
RA	Winterpacht A., Higgins M., Pelletier J., Zabel B.;		
RT	"Identification and characterization of MTR1, a novel gene with		
RT	homology to melastatin (MLSN1) and the trp gene family located in the		
RT	BWS-WT2 critical region on chromosome 11p15.5 and showing allelic-		
RT	specific expression."		
RL	Hum. Mol. Genet. 9:203-216(2000).		
DR	EMBL; AF177473; AAF26288.1; -		
DR	Genew; HGNC:14323; TRPMS.		
DR	GO; GO:0016021; C:integral to membrane; TAS.		
DR	GO; GO:0005216; F:ion channel activity; TAS.		
DR	InterPro; IPR002111; Cat_channel_TrpL.		
DR	InterPro; IPR005821; Ion_trans.		
DR	Pfam; PF00520; Ion_trans; 1.		
KW	Ion transport; Ionic channel; Transmembrane; Transport.		
SQ	SEQUENCE 1165 AA; 131450 MW; C4AD5BAA866BE73B CRC64;		

Query Match 100.0%; Score 6093; DB 2; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MODVQPRPGSGDAEDRRRLGLHGEVNFVGGSGKKRGKFRVPSGAPSVLFDLLAEW	60
DB	1	MODVQPRPGSGDAEDRRRLGLHGEVNFVGGSGKKRGKFRVPSGAPSVLFDLLAEW	60
QY	61	HLPAFLVSVLVEGEQPFAMKSLRDLRLKGLVKAAQSTGAMILTSALRVGLARHVGQAV	120
DB	61	HLPAFLVSVLVEGEQPFAMKSLRDLRLKGLVKAAQSTGAMILTSALRVGLARHVGQAV	120
QY	121	RHSLASTSTKRVAVAGMASLGRVLRHRLLEAEQDFPVHPEDDGGSGGLCSLDSNL	180
DB	121	RHSLASTSTKRVAVAGMASLGRVLRHRLLEAEQDFPVHPEDDGGSGGLCSLDSNL	180
QY	181	SHFLLVEPPGPGKDGGLTELRLRLKHLSEORAGYGTSGTIEIPVLCILVNGDPNTERI	240
DB	181	SHFLLVEPPGPGKDGGLTELRLRLKHLSEORAGYGTSGTIEIPVLCILVNGDPNTERI	240
QY	241	SRAVEQAAPWLILVGGGDIADVLALVNPHLLVPKVAEKQPKFKFSWEDIVRWT	300

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Db 241 SRAVEQAAPWLLVSGGGIADVLALVNQPHLLVPKVAEKQKFKPSPKSHFSEWEDIVMT 300
Qy 301 KLLQNTSHQHLTLTYDFEQSGSEBELDTVILKALVKACKSHSQEPQDYLDLKLAVAWDR 360
Db 301 KLLQNTSHQHLTLTYDFEQSGSEBELDTVILKALVKACKSHSQEPQDYLDLKLAVAWDR 360
Qy 361 VDIKSEIFNGDVEWKSCLDEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYL 420
Db 361 VDIKSEIFNGDVEWKSCLDEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYL 420
Qy 421 SVSRKSLFLLQKQKEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLVKDFLQDACRG 480
Db 421 SVSRKSLFLLQKQKEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLVKDFLQDACRG 480
Qy 481 FYQDGRPDGRRRAEKGPAPKPTGQKWLDDLNQKSENPMRDILFLAVLQNRHEMATYFWAM 540
Db 481 FYQDGRPDGRRRAEKGPAPKPTGQKWLDDLNQKSENPMRDILFLAVLQNRHEMATYFWAM 540
Qy 541 GOEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLV 600
Db 541 GOEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLV 600
Qy 601 RNRKWSKTTCLHLATEADAKAFAHGDVGQAFLTRIMWGDMAAGTPILRLILGAFLLCPALV 660
Db 601 RNRKWSKTTCLHLATEADAKAFAHGDVGQAFLTRIMWGDMAAGTPILRLILGAFLLCPALV 660
Qy 661 YTNLTTFSEAPLRTGLDQLDLSLDTKESPLVGLQSRVSELVEAPRAQGDGRGRAVFL 720
Db 661 YTNLTTFSEAPLRTGLDQLDLSLDTKESPLVGLQSRVSELVEAPRAQGDGRGRAVFL 720
Qy 721 LTRWRKFGAPVTVFLGNVVMYFAPLFTVYLVLDVRRPPQSGSPREVTLYFWVFTLV 780
Db 721 LTRWRKFGAPVTVFLGNVVMYFAPLFTVYLVLDVRRPPQSGSPREVTLYFWVFTLV 780
Qy 781 BEIRQGFPTDETHLVKKFTLYVGNMKNKDMVAIFLFIIVGVTCTRMPLPSAFEAGRTVLAM 840
Db 781 BEIRQGFPTDETHLVKKFTLYVGNMKNKDMVAIFLFIIVGVTCTRMPLPSAFEAGRTVLAM 840
Qy 841 DPMVFTLRLIHFALHKLQGLPKIIVVERMKDQVFFLFLSVLVAQVTTQALLHPHDG 900
Db 841 DPMVFTLRLIHFALHKLQGLPKIIVVERMKDQVFFLFLSVLVAQVTTQALLHPHDG 900
Qy 901 RLEWIFRVLKRPYLQIFQGLPDEIDEARVNCSTHPLLEDSPSCSLYANWLVILLV 960
Db 901 RLEWIFRVLKRPYLQIFQGLPDEIDEARVNCSTHPLLEDSPSCSLYANWLVILLV 960
Qy 961 TFLVTVNVLNLLIAMPSYTFQVVGQADMFVKFQRYNLIVEYHERPALAPPFILLSHL 1020
Db 961 TFLVTVNVLNLLIAMPSYTFQVVGQADMFVKFQRYNLIVEYHERPALAPPFILLSHL 1020
Qy 1021 SLTLRRVPKKAHREHLERDLPDLDQKVVTWETVQENFLSKMEKRRDSEGEVLK 1080
Db 1021 SLTLRRVPKKAHREHLERDLPDLDQKVVTWETVQENFLSKMEKRRDSEGEVLK 1080
Qy 1081 TAHRVDFTAFLYGLLREGEKIKLESQINVCVSVLVSSVADVLAQGGGPRSSQCHGSGSQ 1140
Db 1081 TAHRVDFTAFLYGLLREGEKIKLESQINVCVSVLVSSVADVLAQGGGPRSSQCHGSGSQ 1140
Qy 1141 LVAADHRRGLDQWEPGAGQPPSDT 1165
Db 1141 LVAADHRRGLDQWEPGAGQPPSDT 1165

```

RESULT 2

```

Q9NY34 ID Q9NY34 PRELIMINARY; PRT: 1159 AA.
AC Q9NY34;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE LTRPCS protein (fragment).
GN Name=LTRPCS;

```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Paulsen M., El-Waari O., Engemann S., Franck O., Stroedicke M.,
RA Davies K.R., Bowden L.M., Reinhardt R., Reik W., Harteneck C.,
RA Walter J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270996; CAB66342.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002111; Cat_Channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
DR Ion transport; Ion channel; Transmembrane; Transport.
FT NON_TER 1
SQ SEQUENCE 1159 AA; 130774 MW; E31658EC1125363B CRC64;

Query Match 99.1%; Score 6039; DB 2; Length 1159;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1157; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 9 PGSPGDAEDREILGHRGEVNFSGSKKCKGKFKVRVPSGVAPSVLFDLLLAEMHLPAPNLV 68
Db 1 PGSPGDAEDREILGHRGEVNFSGSKKCKGKFKVRVPSGVAPSVLFDLLLAEMHLPAPNLV 60
Qy 69 VSLVGEQPPAMKSWLDRVLRKGLVKAAQSTGAWILTSALRVGLARHVGAQVDRHSLAST 128
Db 61 VSLVGEQPPAMKSWLDRVLRKGLVKAAQSTGAWILTSALRVGLARHVGAQVDRHSLAST 120
Qy 129 STKRVVAVGMASIGRVLHRRILIEEAQ--EDFPVHYPEDDGGSGQLCSLDSNLSHFILV 186
Db 121 STKRVVAVGMASIGRVLHRRILIEEAQVHEDFPVHYPEDDGGSGQLCSLDSNLSHFILV 180
Qy 187 EPDPPGKGDGLTELRLLEKHIHQAGYCGTGSIEIPVLCLLVNGDPNLTLEISRAVEQ 246
Db 181 EPDPPGKGDGLTELRLLEKHIHQAGYCGTGSIEIPVLCLLVNGDPNLTLEISRAVEQ 240
Qy 247 AAPWLLVSGGGIADVLALVNQPHLLVPKVAEKQKFKPSPKSHFSEWEDIVMTKLIQNI 306
Db 241 AAPWLLVSGGGIADVLALVNQPHLLVPKVAEKQKFKPSPKSHFSEWEDIVMTKLIQNI 300
Qy 307 TSHQHLLTVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDLKLAVAWDRVDIAKS 366
Db 301 TSHQHLLTVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDLKLAVAWDRVDIAKS 360
Qy 367 EIPNGDVEWKSCLDEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYSRSRKS 426
Db 361 EIPNGDVEWKSCLDEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYSRSRKS 420
Qy 427 LLDLQKQKEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLVKDFLQDACRGFYQDGR 486
Db 421 LLDLQKQKEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLVKDFLQDACRGFYQDGR 480
Qy 487 PGDRRRAEKGPAPKPTGQKWLDDLNQKSENPMRDILFLAVLQNRHEMATYFWAMGEGVA 546
Db 481 PGDRRRAEKGPAPKPTGQKWLDDLNQKSENPMRDILFLAVLQNRHEMATYFWAMGEGVA 540
Qy 547 AALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLVRRNCW 606
Db 541 AALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLVRRNCW 600
Qy 607 SKTTCCLHLATEADAKAFAHGDVGQAFLTRIMWGDMAAGTPILRLILGAFLLCPALVYTNLT 666
Db 601 SKTTCCLHLATEADAKAFAHGDVGQAFLTRIMWGDMAAGTPILRLILGAFLLCPALVYTNLT 660
Qy 667 FSEAPLRTGLEDLQDLSLDTKESPLVGLQSRVSELVEAPRAQGDGRGRAVFLTRWRK 726
Db 661 FSEAPLRTGLEDLQDLSLDTKESPLVGLQSRVSELVEAPRAQGDGRGRAVFLTRWRK 720

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QY 727 FWGAPVTVFLGNVVMYFAFLFTYVLLVDRPDPQSGPSEVLYFWVFTLVLEEIRQG 786
 DB 721 FWGAPVTVFLGNVVMYFAFLFTYVLLVDRPDPQSGPSEVLYFWVFTLVLEEIRQG 780
 QY 787 FFTDSDTHLVKKFTLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAPEAGRTVLAQDFWVFT 846
 DB 781 FFTDSDTHLVKKFTLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAPEAGRTVLAQDFWVFT 840
 QY 847 LRLHIFAIHQLGPKIIIVVERMKDVFPEFSLVSMVAVGVTTQALLPHDGRLEWIF 906
 DB 841 LRLHIFAIHQLGPKIIIVVERMKDVFPEFSLVSMVAVGVTTQALLPHDGRLEWIF 900
 QY 907 RRVLYRPVQLQIQPLDIEARVNCSTHPLLEDSPSCPSLYANMLVILLVFLVLT 966
 DB 901 RRVLYRPVQLQIQPLDIEARVNCSTHPLLEDSPSCPSLYANMLVILLVFLVLT 960
 QY 967 NVLLMNLIIAMPSYTFQVQVQGNADMFQVQVNLIVYHERPALAPPFILLSHLSLTURR 1026
 DB 961 NVLLMNLIIAMPSYTFQVQVQGNADMFQVQVNLIVYHERPALAPPFILLSHLSLTURR 1020
 QY 1027 VPKKAHREHLERDLDPDLQKVVWTVQKFNFLSKMEKRRDSEGEVLKTAHRVD 1086
 DB 1021 VPKKAHREHLERDLDPDLQKVVWTVQKFNFLSKMEKRRDSEGEVLKTAHRVD 1080
 QY 1087 FTAKYLGGLREOEKRIKLESQINVCVSVVADVLAQGGGPRSSQHCQEGSOLVAADH 1146
 DB 1081 FTAKYLGGLREOEKRIKLESQINVCVSVVADVLAQGGGPRSSQHCQEGSOLVAADH 1140
 QY 1147 RGGLDGEQPGAGQPPSDT 1165
 DB 1141 RGGLDGEQPGAGQPPSDT 1159

RESULT 3
 Q9JUH7
 ID Q9JUH7 PRELIMINARY; PRT; 1158 AA.
 AC Q9JUH7
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE MSLN1-and TRP-related protein 1 (MTR1) (Transient receptor potential
 cation channel subfamily M member 5).
 GN Name=Trpm5; Synonyms=Mtr1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20363096; PubMed=10907850;
 RA Yatsuki H., Watanabe H., Hattori M., Joh K., Soejima H., Komoda H.,
 RA Xin Z., Zhu X., Higashimoto K., Nishimura M., Kuratomi S., Sasaki H.,
 RA Sakaki Y., Mukai T.;
 RT "Sequence-based structural features between Kv1qt1 and Tapal on mouse
 chromosome 7p4/p5 corresponding to the Beckwith-Wiedemann syndrome
 region on human 1p15.5: long-stretches of unusually well conserved
 intronic sequences of kv1qt1 between mouse and human.";
 RL DNA Res. 7:195-206 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20366135; PubMed=10903843; DOI=10.1006/geno.2000.6234;
 RA Enklaar T., Esswein M., Oswald M., Hilbert K., Winterpacht A.,
 RA Higgins M., Zabel B., Prawitt D.;
 RT "Mtr1, a novel biallelically expressed gene in the center of the mouse
 distal chromosome 7 imprinting cluster, is a member of the Trp gene
 family.";
 RL Genomics 67:179-187 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=129/SvxC57BL; TISSUE=Lung;
 RC MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
 RA Hofmann T., Chubakov V., Gudermann T., Montell C.;
 RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent

selective cation channel.";
 Curr. Biol. 13:1153-1158 (2003).
 DR EMBL; AB019952; BAA96877.1; -
 DR EMBL; AF228681; AAF98120.1; -
 DR EMBL; AY280364; AAP44476.1; -
 DR MGD; MGI:1861718; Irpm5.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005261; F: cation channel activity; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0006812; P: cation transport; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Ion_trans; 1.
 DR PRINTS; PR01415; ANKYRIN.
 KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
 SQ SEQUENCE 1158 AA; 130843 MW; FOA5237EC67867CE CRC64;

Query Match 83.5%; Score 5088.5; DB 2; Length 1158;
 Best Local Similarity 84.1%; Pred. No. 0;
 Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

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 DB 1 MOTTQSSCPGPPPTDDEGWEPILCRGEINFGSGKRGKFKVPSVAPS VLFLLLTETW 60
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 DB 61 HLPAPNLVSVLGVGEERPLAMKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGOAV 120
 QY 121 RDHSLASTSTKVRVAVGVAMASLGRVLRHRIIE--EAQEDFPVHPEDDGGSGGGLCSLDS 178
 DB 121 RDHSLASTSTKIRVVAIGMASLDRILHRQLLDGVHQKEDTPIHYPADEGNIQGGLCLDS 180
 QY 179 NLSHPILVERPPGKG-DGLTELRLRLEKHSERAGYGGTGSTIIPVLCLLVNGDPNTL 237
 DB 181 NLSHPILVESGALGSGNDGLTELQSLSEKHSIQORTGYGGTSCIQIPVLCLLVNGDPNTL 240
 QY 238 ERISRAVEQAAPWLLITVSGGIGADVLAALVNPQPHLLVPKVAEKQFKPKFSPKSHFSEWIDV 297
 DB 241 ERISRAVEQAAPWLLITAGSGIGADVLAALVNPQPHLLVPKVAEKQFKPKFSECFSEWIAIV 300
 QY 298 RWTLLQNTISHOHLITVYDFEQEGSEELDTVILKALVKACKSHSQEODYLDLKLAVA 357
 DB 301 HWTLLQNTIAAHPHLLITVYDFEQEGSELDITVILKALVKACKSHSQEADYLDLKLAVA 360
 QY 358 WDRVDIAKSEIFNGDVEWVKSCDLEEWYDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 417
 DB 361 WDRVDIAKSEIFNGDVEWVKSCDLEEWYTDALVSNKPDFVRLFDVSDGADMAEFLTYGRLOO 420
 QY 418 LYRSVSRKSLFLDLLQKQOEARLTLAGLGTQQAEPAGPPAFSLHEVSRVLKDFLODA 477
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 QY 478 CRGFYQDGRPGDRRAEAKPRAKPTGQKWLDDLNOKSNPNWRDLFLMAVLQNRHEMATYF 537
 DB 481 CRGFYQDQ-----RRMEERGPAPKPAQKWLPLSRKSDPWRDLFLMAVLQNRHEMATYF 536
 QY 538 WAMQEGVAAALAAACKILKEMSHLSEAEAPATREAKYERLALDLFSECYNSSEARAPA 597
 DB 537 WAMQEGVAAALAAACKIEMSHLEKEAEVARTMEAKYEQALDLFSECYNSSEARAPA 596
 QY 598 LLVVRNCRWKTTCILHLATEADAKAFFAHGDVQOAFTRIWMGDMAAGTPIRLGLAFLCP 657
 DB 597 LLVVRNHSRSTTCILHLATEADAKAFFAHGDVQOAFTRIWMGDMAAGTPIRLGLAFLCP 656
 QY 658 ALVYTNLITFSEAPLRTGLEDLQDLSDLTSEKSPLYGLQSRVEELVEAPRAGQGRGPPA 717
 DB 657 ALIYTNLITFSEDAQPMQDLEQLQPSDLDMEKSLCSRGQGLEKLEATEAPRAGDLPQA 716
 QY 718 VFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDRPDPQSGPSEVLYFWVFT 777
 DB 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDRPDPQSGPSEVLYFWVFT 776

QY 778 LVLEIRQGFDTDETHLVKFTLYVGDNNKCDMVAIFLFIYGVTCRMLPSAFEAGRTV 837
 Db 777 LVLEIRQGFDTDETHLVKFTLYVEDNNKCDMVAIFLFIYGVTCRMVPSFEAGRTV 836
 QY 838 LAMDPMVFTLRILHIFAIHQGLGPKIIVVERMKDVFFLFFLSVWLVAIVGVTQALLHP 897
 Db 837 LAIDPMVFTLRILHIFAIHQGLGPKIIVVERMKDVFFLFFLSVWLVAIVGVTQALLHP 896
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 Db 897 HDGRLEWIFRRVLYRYPYLIQFGQIPDEIDARVNCSTHPLLEDSPSPSYANWLVIL 956
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 Db 957 LLVTFLLVTNVLNLLIAMFSYTFQVQGNADMFVKFQRYNLIYVYHERPALAPPFILL 1016
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 Db 1017 SHLSLTLRRVPKKEAEKREHLERDLPDLDQKVWTWVQKFNFLSKMEKRRRDSGEV 1076
 QY 1078 LRKTAHRVDIFIAKYLGLREQEKRIKLESQINYSVLVSSVADVLAAOGGPRSSQHCGE 1137
 Db 1077 LRKTAHRVDLIAKYIGLREQEKRIKLESQINYSVLVSSVADVLAAOGGPRSSQHCGE 1136
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 Db 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 4
 Q9EPM4 PRELIMINARY; PRT; 1148 AA.
 AC Q9EPM4;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Ltrpc5 protein.
 GN Name=lrpm5; Synonyms=Ltrpc5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RX PubMed=10915772; DOI=10.1093/hmg/9.12.1829;
 RA Paulsen M., El-Mearri O., Engemann S., Stroedicke M., Franck O.,
 RA Davies K., Reinhardt R., Reik W., Walter J.;
 RT "Sequence conservation and variability of imprinting in the Beckwith-
 RT Wiedemann syndrome gene cluster in human and mouse.";
 RL Hum. Mol. Genet. 9:1829-1841(2000).
 DR EMBL; AJ251835; CAC19456.1; -.
 DR MGD; MGI:1861718; Trpm5.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat.channel_TrpL.
 DR InterPro; IPR005821; Ion.trans.
 DR Pfam; PF00520; Ion.trans.
 DR PRINTS; PR01415; ANKVRIN.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 1148 AA; 129630 MW; 947AF5B9CFDCA127 CRC64;

Query Match 82.7%; Score 5036.5; DB 2; Length 1148;
 Best Local Similarity 85.5%; Pred. No. 0;
 Matches 966; Conservative 63; Mismatches 94; Indels 7; Gaps 3;
 QY 1 MQDVGGPPGSGDAEDRELGLRGVNFVGGSGKRGKRVPSGVAPSLFDLLAEW 60
 Db 1 MQTVSSCFGPPDTEGWEPILCRGTEINFGSGKRGKRVPSGVAPSLFELLITW 60

QY 61 HLPAPNLVSVLVBGEQPFAMKSWLRDVLRLKGLVKAAQSTGAWILTSALRYGLARHVQAV 120
 Db 61 HLPAPNLVSVLVBGEQPFAMKSWLRDVLRLKGLVKAAQSTGAWILTSALRYGLARHVQAV 120
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 Db 121 RDHSLASTSTKRVVAVCMASLGRVLAHRRILE--EAGEDFPVHYPEDGSGQPLCLSDS 180
 QY 179 NLSHFILVEPPGPKG-DGLTELRRLRLEKHSIORAGYGGTGTETIPVLCLLVNGDDNTL 237
 Db 181 NLSHFILVESGALSGNDGLTELQLSLEKHSIORAGYGGTGTETIPVLCLLVNGDDNTL 240
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 Db 241 ERISRAVQQAAPWILLVSGGSIADVLAAVNPQPHLLVPKVAEQKFKSPKSHFSMEDIV 300
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 Db 301 HWTLLQNIIAHPHLLTVYDPEOGBSELDTVILKALVKACKSHSOBQDYLDELKAVA 360
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 QY 418 LYRSVSRKSLFLDLQKQKQEARLTLAGLGTQOAREPPAGPPAFPSLHESRVVLKDFLODA 477
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 Db 481 CRGFYQDGRFRRRAEKGPFAKPTQKWLILLNQSENPNWRDLFLWAVLQNRHWMATYF 536
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 Db 657 ALVYTNLIITFSEAPLRTGLEDLQDLSDLTBKSPLYGLQSRVEELVEAPRAGQGRGPA 716
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 Db 717 AFLTRWRKFWGAPVTVFIGNVVMYPAFLFTYTVLLVDPRPPQPSGPEVTLYFWVPT 776
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 Db 777 LVLEIRQGFDTDETHLVKFTLYVGDNNKCDMVAIFLFIYGVTCRMLPSAFEAGRTV 836
 QY 838 LAMDPMVFTLRILHIFAIHQGLGPKIIVVERMKDVFFLFFLSVWLVAIVGVTQALLHP 897
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 Db 1077 LRKTAHRVDLIAKYIGLREQEKRIKLESQINYSVLVSSVADVLAAOGG 1126

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RESULT 5
Q99NF9 PRELIMINARY; PRT; 1148 AA.
ID Q99NF9;
AC Q99NF9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ltrp5 protein.
GN Name=Trpms5; Synonyms=Ltrp5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX PubMed=10915772; DOI=10.1093/hmg/9.12.1829;
RA Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O.,
RA Davies K., Reinhardt R., Reik W., Walter J.;
RT "Sequence conservation and variability of imprinting in the Beckwith-
RT Wiedemann syndrome gene cluster in human and mouse.";
RL Hum. Mol. Genet. 9:1829-1841(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RA Engemann S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271092; CAB94717.2; -.
DR MGD; MGI:1861718; Trpm5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR005821; Ion trans.
DR Pfam; PF00520; Ion trans. 1.
DR PRINTS; PR01415; ANKXRN.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW ION TRANSPORT; IONIC CHANNEL; TRANSMEMBRANE; TRANSPORT.
SQ SEQUENCE 1148 AA; 129590 MW; 90517E8557DCA127 CRC64;

Query Match 82.5%; Score 5026.5; DB 2; Length 1148;
Best Local Similarity 85.4%; Pred. No. 0;
Matches 965; Conservative 63; Mismatches 95; Indels 7; Gaps 3;

QY 1 MQDVQGRPGSGDAERELGHRGEVNPFGSGKRGKFRVPSGVAISVLPDLIAEW 60
DB 1 MQTTQSCPGSPDTEGWEPILCRGEINFGSGKRGKFRVPSVAPSVLPFELLTEW 60

QY 61 HLPAPNLVSLVGEERPFANKSWLRDVLKGLVKAQSTGAWILTSALRVGLARHVGQAV 120
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QY 121 RDHSLASTSKRVAVAGMASLGRVLRILE--EAQEDPPVHYVEDDGGSGPLCSLDS 180
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QY 179 NLSHFILVPEPGKGG--DGLTELRLKLEKHSIQAGYGTGSIPIVCLLVNGDPNTL 237
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QY 181 NLSHFILVPEPGKGG--DGLTELRLKLEKHSIQAGYGTGSIPIVCLLVNGDPNTL 240
DB 181 NLSHFILVPEPGKGG--DGLTELRLKLEKHSIQAGYGTGSIPIVCLLVNGDPNTL 240

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QY 361 WDRVDIAKSEIFNGDVEWKSCDLEVMVMDALVSNKPFVRLFVDNGADVADFLTYGRLOE 420
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QY 418 LYRSVSRKSLFDLLQRLQKQEERLTLAGLGTQQAQREPPAGPPAPSLHEVSRVLKDFLQDA 477
DB 418 LYRSVSRKSLFDLLQRLQKQEERLTLAGLGTQQAQREPPAGPPAPSLHEVSRVLKDFLQDA 477

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DB 421 LYHSVSPKSLFELLQKHEGRITLAGLGAQQAARELPIGLPAPSLHEVSRVLKDFLQDA 480
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DB 481 CRGYQGRPGDRRAAEKGPAPKPTGOKWLLDLNKSSEPNWRDLFLWAVLQNRHEMATYF 536
QY 538 WAMQEGVAAALAAACKILKEMSHLETEAEARATREAKYERLALDLSECSYNSSEARAF 597
DB 537 WAMQEGVAAALAAACKILKEMSHLETEAEARATREAKYERLALDLSECSYNSSEARAF 596
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DB 657 ALVVTNLITFSEAPLRTGLDQLDLSLDTSEKSPLYGLQSRVRELVEAPRAQDGRGPA 716
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DB 717 VFLTRWRKFWGAPVTVFLGNVVFAPLFTVTVLLVDFRPPPGQSPGSEVTLFWYFT 776
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DB 777 LVLEBIROGFTTDETHLVKKFTLYVGNWNKCDMAIFLFTVGTCTRMVPSVFEAGRTV 836
QY 838 LAMDPMVFTLRIHIFATHKOLGPKIIIVERMKDKVFFFLFSLVWLVAYGVTTQALLHP 897
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DB 897 HDGRLEWIFRRVLYRYPYLQIFGQIPDLDEIDARVNCSTHPLLEDSPSCPSLYANWLVL 956
QY 958 LLVTFELVTNVLMLLIAMFSYTPQVQGNADMFQKQRYNLIIVEYHERPALAPPFILL 1017
DB 957 LLVTFELVTNVLMLLIAMFSYTPQVQGNADMFQKQRYNLIIVEYHERPALAPPFILL 1016
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DB 1017 SHLSLTLRRVFKAEKREHLERLDPDLPDQKVVTWETQKFNFLSKMKERRRSEGEV 1076
QY 1078 LRKTAHRVDFTAKYLGGLREQEKRICKLESQINYSVLVSSVADVLAQGG 1127
DB 1077 LRKTAHRVDFTAKYLGGLREQEKRICKLESQINYSVLVSSVADVLAQGG 1126

RESULT 6
Q9EPM3 PRELIMINARY; PRT; 1116 AA.
ID Q9EPM3;
AC Q9EPM3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ltrp5 protein.
GN Name=Trpm5; Synonyms=Ltrp5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX PubMed=10915772; DOI=10.1093/hmg/9.12.1829;
RA Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O.,
RA Davies K., Reinhardt R., Reik W., Walter J.;
RT "Sequence conservation and variability of imprinting in the Beckwith-
RT Wiedemann syndrome gene cluster in human and mouse.";
RL Hum. Mol. Genet. 9:1829-1841(2000).
DR EMBL; AJ251835; CAC19457.1; -.
DR MGD; MGI:1861718; Trpm5.
GO; GO:0016021; C:integral to membrane; IEA.

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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RC TISSUE=Embryonic body between diaphragm region and neck;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasakawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akaiura S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK035197; BAC28976.1;
 DR MGD; MG1:1861718; Trpm5.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005261; P: cation channel activity; IEA.
 DR GO; GO:0004872; P: receptor activity; IEA.
 DR GO; GO:0006812; P: cation transport; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat channel_TrlpL.
 DR Pfam; PF00520; Ion trans. 1.
 DR PRINTS; PR01415; ANKRYIN.
 KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
 FT NON_TER 1
 SQ SEQUENCE 1030 AA; 116983 MW; DDB31B7DF238F402 CRC64;

Query Match 73.3%; Score 4465.5; DB 2; Length 1030;
 Best Local Similarity 84.4%; Pred. No. 5.8e-290;
 Matches 858; Conservative 56; Mismatches 91; Indels 11; Gaps 3;

QY 151 LBEAQDFPVHYPEDDGSGGQPLCSLDSNLSHFLFVPEPGKG-DGLTELRLRLEKHS 209
 DB 25 LSLAQEDTHIHPADSGNIQGPLCLDSNLSHFLVESGALSGNDGLTELQSLSEKHS 84
 QY 210 EQRAGYGGTGSIEIPVCLLVNGDPNTERISRAREQAAPWLLVSGGIAVLALVNO 269
 DB 85 QQRTGYGGTSCIQIPVCLLVNGDPNTERISRAREQAAPWLLVSGGIAVLALVNO 144
 QY 270 PHLLVPKVAEKQPEKFPKSHGWEDIVRWTKLQNTSHQHLTVYDFEQSGSELDTV 329
 DB 145 PHLLVPQVAEKQPEKFPKSHGWEDIVRWTKLQNTSHQHLTVYDFEQSGSELDTV 204
 QY 330 ILKALVKAKSHQEQPDYLDLKLAVMDRVDAIAKSEIFNGDVWVKSCDLSEVMDALV 389
 DB 205 ILKALVKAKSHQEQPDYLDLKLAVMDRVDAIAKSEIFNGDVWVKSCDLSEVMDALV 264
 QY 390 SNKPEFVRLVFDNGADVADFTYGRLOELVRSVRSKSLFLPDLQRQKEARLTLAGLGTQ 449
 DB 265 SNKPDFVRLVFDNGADVADFTYGRLOELVRSVRSKSLFLPDLQRQKEARLTLAGLGTQ 324
 QY 450 QAREPPAGPAPFSLHVSRLVKDPLQDACGFGYODGPGDRRAEKGAPKRPQGWKLLD 509
 DB 325 QAREPLIGLPAFSLHVSRLVKDPLQDACGFGYODGPGDRRAEKGAPKRPQGWKLLD 380
 QY 510 LNKSENPNPDLFLWALQNRHEMATYFWAMQEGVAAALAAACKILKEMSHLSEAEAR 569
 DB 381 LSRKSEDPWRDLFLWALQNRHEMATYFWAMQEGVAAALAAACKILKEMSHLSEAEAR 440

QY 570 ATREAKYERLALDLFSECYSNSEARAFALLVRRNRCWKTTCGLHATEADAKAFHAGV 629
 DB 441 TMREAKYEQALDLFSECYNSSEARAFALLVRRNHSRRTTCLHATEADAKAFHAGV 500
 QY 630 QAFUTRIWGDMAAGTPIILLGALFPCALPVYNTLITFSEAPLRTGLEDLQDLSLDTE 689
 DB 501 QAFUTKIWGDMAAGTPIILLGALFPCALPVYNTLITFSEAPLRTGLEDLQDLSLDTE 560
 QY 690 KSPLYGLQSVREELVAPRAQGRGPRVALLTRKFWGAPVTVFLGNVVMYFAFLFLF 749
 DB 561 KSFLCSRGQGLQTEAPRAPDGLGPOAFLTRKFWGAPVTVFLGNVVMYFAFLFLF 620
 QY 750 TYVLLVDFRPPPGQSPGVTVLYFWVTVLVEEIRQGFTEDETHLVKKFTLYVGDNNWK 809
 DB 621 TYVLLVDFRPPPGQSPGVTVLYFWVTVLVEEIRQGFTEDETHLVKKFTLYVEDNNWK 680
 QY 810 CDWVAIFLFIIVGVTCTMLPSAFAGRTVLAIDMFWVTLRLHIHFAIHKQLGPKLIIVERM 869
 DB 681 CDWVAIFLFIIVGVTCTMLPSAFAGRTVLAIDMFWVTLRLHIHFAIHKQLGPKLIIVERM 740
 QY 870 MKDVFFFLFSLVWLVAYGVTTQALLPHDGRLEWIFRRVLYRYPVLOIFGOIPDEIDEA 929
 DB 741 MKDVFFFLFSLVWLVAYGVTTQALLPHDGRLEWIFRRVLYRYPVLOIFGOIPDEIDEA 800
 QY 930 RVNGSTHPLLEDSPSCPSLYANWLVLLVTFLLVTNVLNLLIAMFSTFQVQVQNA 989
 DB 801 RVNCSLHPLLEDSPSCPSLYANWLVLLVTFLLVTNVLNLLIAMFSTFQVQVQNA 860
 QY 990 DMFWKQRYNLIVYHERPALAPPFILLSHLSLTLRRVFKKEAEKREHLERDLPLDQ 1049
 DB 861 DMFWKQRYNLIVYHERPALAPPFILLSHLSLTLRRVFKKEAEKREHLERDLPLDQ 920
 QY 1050 KVVTWETVQENFLSKMKERRRDSGEVLRKTAHRVDPIAKYVGLGRQEKRIKLESQI 1109
 DB 921 KIITWETVQENFLSKMKERRRDSGEVLRKTAHRVDPIAKYVGLGRQEKRIKLESQI 980
 QY 1110 NVCSVLVSSVADVLQAQGGPRSSQCGSGSLVLAADHRGGLDGMWEPQGPQPPST 1165
 DB 981 NYCMLLSMTDTLAPGQTYSSQCGSCRSQASARDREYLE-----SGLPPSDT 1030

RESULT 8
 QYTP4
 ID Q7TFL4 PRELIMINARY; PRT; 1000 AA.
 AC Q7TFL4;
 DT 01-OCT-2003 (TREMREL. 25, Created)
 DT 01-OCT-2003 (TREMREL. 25, Last sequence update)
 DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
 DE Transient receptor potential cation channel subfamily M member 5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvxC57BL; TISSUE=Testis;
 RC MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
 RA Hofmann T., Chubnov V., Gudermann T., Montell C.;
 RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent
 RT selective cation channel.";
 RL Curr. Biol. 13:1153-1158(2003).
 DR EMBL; AY280365; RAP44477.1;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005261; P: cation channel activity; IEA.
 DR GO; GO:0004872; P: receptor activity; IEA.
 DR GO; GO:0006812; P: cation transport; IEA.
 DR InterPro; IPR002111; Cat channel_TrlpL.
 DR InterPro; IPR005821; Ion trans.
 KW Pfam; PF00520; Ion trans; 1.
 SQ SEQUENCE 1000 AA; 112459 MW; BB107610176E6660 CRC64;

Query Match		71.5%; Score 4354.5; DB 2; Length 1000;
Best Local Similarity		84.4%; Pred. No. 1.5e-282;
Matches		842; Conservative 53; Mismatches 92; Indels 11; Gaps 4;
Qy	1	MDVQGRPPGSGDAEDRRLGLHRRGEVNFPGSGKRGKRVVPVSGVAPSVLFDLLASW 60
Db	1	MDVQGRPPGSGDAEDRRLGLHRRGEVNFPGSGKRGKRVVPVSGVAPSVLFDLLASW 60
Qy	61	HLAPNLVSLVGEOPFAMKSWRLVLRKGLVKAAQSTGAWILTSALRVGLARHVQAV 120
Db	61	HLAPNLVSLVGEOPFAMKSWRLVLRKGLVKAAQSTGAWILTSALRVGLARHVQAV 120
Qy	121	RDHSLASTSKRVAVGASLGRVLRHRIE--EAQEDFPVHYPPDDGSGSPCLSDS 178
Db	121	RDHSLASTSKRVAVGASLGRVLRHRIE--EAQEDFPVHYPPDDGSGSPCLSDS 178
Qy	179	NLSHFILVEPGPGKG-DGLTEURLRLEKHSERAGYGGTGSIEIPVLCILVNGDPNTL 237
Db	181	NLSHFILVSGALSGNDGLTELQSLKHSIQRTGYGGTGTCTIPIVLCILVNGDPNTL 240
Qy	238	ERISRAVEQAAPWLLILVSGGIADVLAAVNPHLLVPKVAEKQKEKPPSKHFWEDIV 297
Db	241	ERISRAVEQAAPWLLILVSGGIADVLAAVNPHLLVPKVAEKQKEKPPSKHFWEDIV 297
Qy	298	RWTKLLQNTSHOHLTVYDFQSGSEELDTVLKALKACKSHSQEPQDYDELKLAVA 357
Db	301	HMTTELLQNTAAHPHLLTVYDFQSGSEELDTVLKALKACKSHSQEAQDYDELKLAVA 360
Qy	358	WRVDIAKSEIFNGDVEWKSCLDEEVMVDALVSNKPEFVRLVFDNGADVADPLTYGRLOE 417
Db	361	WRVDIAKSEIFNGDVEWKSCLDEEVMVDALVSNKPEFVRLVFDNGADVADPLTYGRLOE 420
Qy	418	LYRSVSRKSLDLQKQKOEAEALTLAIGLTQQAEPAGPAPFSLVSVRLKDFLQDA 477
Db	421	LYHSVSPKSLFELLQKHEEGRLTLAIGLGAQQAELPILGAPFSLVSVRLKDFLQDA 480
Qy	478	CRGFYQDGPGRRRABKGPAPGTQKWLIDLNOKSNPWRDLFLMAVLQNRHETATYF 537
Db	481	CRGFYQDG---RRMEERGPGRAPQKQWLPDLRSKSDPNRDLFLMAVLQNRHETATYF 536
Qy	538	WAMQGVAAALAAACKIKEMSHLATEAARATREAKYERLADLSECYNSSEARAF 597
Db	537	WAMQGVAAALAAACKIKEMSHLATEAARATREAKYERLADLSECYNSSEARAF 596
Qy	598	LLVRNRCSWKTCLHLATEADAKAFFAHGQVQAFILTRIMWGMAGTPILRLLGATCP 657
Db	597	LLVRNRCSWKTCLHLATEADAKAFFAHGQVQAFILTRIMWGMAGTPILRLLGATCP 656
Qy	658	ALVYTNLITFSEAPLRTGLEDLQSLDTEKSLYGLQSRVELVEAPRAQGDGPRA 717
Db	657	ALVYTNLITFSEAPLRTGLEDLQSLDTEKSLYGLQSRVELVEAPRAQGDGPRA 716
Qy	718	VELLTRWRKFWGAPVTVLGNVVMYFAFLFTYVLLVDRPPQSGSPRVTLVFWFT 777
Db	717	VELLTRWRKFWGAPVTVLGNVVMYFAFLFTYVLLVDRPPQSGSPRVTLVFWFT 776
Qy	778	LVLEIRQGFDETHLVKFTLVYVGNWKNKDMVAIFLFIIVGVTCTMLPFAEGRTV 837
Db	777	LVLEIRQGFDETHLVKFTLVYVGNWKNKDMVAIFLFIIVGVTCTMLPFAEGRTV 836
Qy	838	LAMDPMVFTLRLIHLFAHKGPKIIVVERMKDVFPLFLFLSVLVAVGVTTQALLHP 897
Db	837	LAMDPMVFTLRLIHLFAHKGPKIIVVERMKDVFPLFLFLSVLVAVGVTTQALLHP 896
Qy	898	HGRLWIFRVLVRPVLQIFQIPLDEIDEARVNCSTHPLLLSDSPSCSLYANMLVIL 957
Db	897	HGRLWIFRVLVRPVLQIFQIPLDEIDEARVNCSTHPLLLSDSPSCSLYANMLVIL 956
Qy	958	LLVTFLLVTNVLNMLLIAMSYFQVQGNADMFVKF 995
Db	957	LLVTFLLVTNVLNMLLIAMSYFQVQGNADMFVKF 990

RESULT 9	
ID	Q8TD43
AC	Q8TD43
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Cation channel TRPM4B (Transient receptor potential ion channel melastatin subgroup member 4 protein) (Transient receptor potential cation channel subfamily M member 4 splice variant B).
DE	Name=TRPM4B; Synonyms=TRPM4;
GN	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22011788; PubMed=12015988; DOI=10.1016/S0092-8674(02)00719-5;
RA	Launay P., Fleig A., Perraud A.L., Scharenberg A.M., Penner R.,
RA	Kinet J.P.;
RT	"TRPM4 is a Ca2+-activated nonselective cation channel mediating cell membrane depolarization.";
RT	Cell 109:397-407(2002).
RL	[2]
RP	SEQUENCE FROM N.A.
RX	Perraud A.-L., Scharenberg A.;
RA	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;
RX	MEDLINE=22791733; PubMed=12799367; DOI=10.1074/jbc.M305127200;
RA	Nilius B., Prenen J., Droogmans G., Voets T., Vennekens R.,
RA	Freichel M., Wassenbach U., Flockert V.;
RT	"Voltage dependence of the Ca2+ activated cation channel TRPM4.";
RL	J. Biol. Chem. 278:30813-30820(2003).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
RA	Hofmann T., Chubakov V., Gudermann T., Montell C.;
RT	"TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent selective cation channel.";
RT	Curr. Biol. 13:1153-1158(2003).
DR	EMBL; AF497623; AAM18083.1; -
DR	EMBL; AJ575813; CAE05941.1; -
DR	EMBL; AY297045; AAP44474.1; -
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0005261; F:cation channel activity; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0006812; P:cation transport; IEA.
DR	InterPro; IPR002111; Cat channel_TrpL.
DR	InterPro; IPR005821; Ion trans. 1.
DR	Pfam; PF00520; Ion trans. 1.
KW	Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
SQ	SEQUENCE 1214 AA; 134300 MW; 76ADA452690ED8F5 CRC64;
Query Match	
Best Local Similarity 40.2%; Score 2448.5; DB 2; Length 1214;	
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps	
Qy	26 GEVNFQGGKKGKRVVPVSGVAPSVLFDLLAEHLPAPNLVSLVGEOPFAMKSWLR
Db	76 GELDTGAGRKSHNPLRLSDRTDPAAVYSLVTRTWGFRAPNLVSVLGGSPVLQTLQ
Qy	86 DVLRKGLVKAQSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVAVAGVMSLRV
Db	136 DLLRGLVKAQSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVAVAGVMSLRV
Qy	146 LHRRILEAQEDFPVHY-----PEDDGGSGPLCSLSDNLSHFIIVPEPGKGDGLTEL
Db	195 RNRDTLNPKGSPFARYRWGRDPPD--GVQFP---LDYNSAFFLVDDGTHGCLGENRF
Qy	201 RLRLKHLSEQRAGYGGTGSIEIPVLCILVNGDPNTLERISRVAEQAAPWILVSGSGIA

Db 250 RLRLSYISQKQTVGGTG-IDIPVLLLLIDGDEKMLTRIENATQAOLPCLLVAGSGAA 308
Qy 261 DVLAALVNQPHLLVP-----KVAEKQFKEKPSKSHSWEDIVRWTKLLQNTSHQHL 313
Db 309 DCLAEITLED--TLAPSGGARAGEARDIRRFPPK-----GDLEVLQAOVERIMTRKELL 361
Qy 314 TVYDFEQRSGSELDIVILKALVKACKSHSQPDYLDLKLAVADRWVDIAKSHIFNGDV 373
Db 362 TVYSSE-DGSEEFETIVILKALVKAC--GSSEASAVLDELRLAVANRWVDIAQSEIFRGI 418
Qy 374 EWKSCDLEVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYSRVSRLKLLFDLQ 433
Db 419 QWRSHLEASLMDALLNDRPEFVRLLIHGLSLGHFLTPMLRLAQLYSAAPNSLIRNLLD 478
Qy 434 RKQEARLITLAGL--GTQOAREPPAGPAPFSLHESVRLVKDFLODACRGFFQDGRPGDR 491
Db 479 QASHSAGTKAPALKGAELRPP-----DVGHVRLMLLGGKCAPRPSGGAWDPH 528
Qy 492 RAEGKPAKRPCTQKWLDDLNQK-----ENPWRDLFWAVLQNRHEMATYFWAMQ 542
Db 529 -----PGQFGEWYLLSDKATSPSLDAGLQOAPWSDLLWALLNRAQWYFWENG 583
Qy 543 EGVAALAAACKILKEMSHLETAEAARATREA--KYERLALDLPSECYSNSEARAFALLV 600
Db 584 NAVSSALGACLLRLVWARLEPDAEAEARRKDLAFKFGMGVDFGECYRSSEVRAARLL 643
Qy 601 RNRCSWKTTCILHATEADAKAFFAHGVOAELTRIMWGDMAAGTPILLRLLGAFICPALV 660
Db 644 RRCPLMGATCQLQAMQADARAFFAQGVQSLLTKQWGDMASTTPIWALVLAFFCPPLI 703
Qy 661 YTNLITF--SEAPLRTGLDQLDLSLDTKSPLYGLQSRVEELVEAPRAQGD----- 712
Db 704 YTRLITFRKSEPTREELE--FDMDSVINGCPGTADPAEKTPGVPRQSGRPGCCGG 761
Qy 713 --RGPRAVPLLRKFWGAPVTFLGNVVMYFAFLFLLFYVLLVDPRPPQSGPEVT 770
Db 762 RCGGRCC--LRWFHFWGAPVTIFMGNVSVYLLFLLFSLRVLVDFQAP--PGSLELL 816
Qy 771 LFWVFTLVLEIRQGFDTEDT-----HLVKKFTLYVGDNNKCDMVALFLFI 819
Db 817 LYFWAFTLLCELRQGLSGGGSLASGGPGCHASLSQRRLYLADSNQCDLVALTCFL 876
Qy 820 VGVTCMLPSAEAGRTVLAMPVFTLRLIHLFAHKOLGPKIIVVERMKDVPPFFLF 879
Db 877 LGVGGCKLTPLGLHLGRTVLICIDFMVFTVRLHLHFTVNNKQLGPKIIVSKMKDVFFLF 936
Qy 880 LSVLVVAYGVTTQALHHDGRLEWIFRRVLYRPYLQIFQIPLDIBEARV---NCSTH 936
Db 937 LGVWLVAVGAVTEGLLRPRDSOPPSILRRVFRPYLIQIFQIPEQDMVALMEHNSCSSE 996
Qy 937 PLLLEDSP-----SCPSLVANMLVLLVTLFLLVNVLLMULLIAMFSYTFQVQGNADM 991
Db 997 PGWAPHPGAQAQCTCVSQVANMLVLLVLLVFLVANILLVLLIAMFSYTFQVQGNADL 1056
Qy 992 FKKFQRYNLIVEHERPALAPPELLSHLSLTLRRVFKK-----EAEKREHLERD 1042
Db 1057 YNKAQRYLITREFSHRPAALAPPVIVISHURLLRLLQRCRPSQPSPALHPRVYLSKE 1116
Qy 1043 LPDPLQKVVMTVQENFLSKWEKRRDSEGEVLRTAHRVDFIAKYLGLRQEQRKI 1102
Db 1117 -----AERKLLTWESVHKEFLARARDKRESDESRLKRTSQKVDLALKQLGHIREVEQRL 1172
Qy 1103 KCLESQINYSVLVSSVADVLAQG-----GGP 1129
Db 1173 KVLEREVQCSRVLGWVAEALSRSALIPPGGP 1204

RESULT 10

Q7TN37

ID

AC

Q7TN37

DT

01-OCT-2003

(T-REMBurel. 25, Created)

DT

01-OCT-2003

(T-REMBurel. 25, Last sequence update)

DT 01-MAR-2004 (T-REMBurel. 26, Last annotation update)
DE Transient receptor potential ion channel melastatin subgroup member 4
DE protein.
GN Name=trpm4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SVJ129; TISSUE=Heart;
RX MEDLINE=22791733; PubMed=12799367; DOI=10.1074/jbc.M305127200;
RA Nilius B., Prenen J., Droogmans G., Voets T., Vennkens R.,
RA Feilchel M., Wissenbach U., Flockerzi V.;
RT "Voltage dependence of the Ca2+ activated cation channel TRPM4.";
EL J. Biol. Chem. 278:30813-30820(2003).
DR EMBL; AJ575814; CAB05940.1; -
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005262; F:calcium channel activity; IDA.
DR GO; GO:0006816; P:calcium ion transport; IDA.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
SQ SEQUENCE 1213 AA; 135759 MW; E4959F53ED35FB66 CRC64;

Query Match 39.4%; Score 2399.5; DB 2; Length 1213;

Best Local Similarity 43.6%; Pred. No. 1.8e-151;

Matches 530; Conservative 185; Mismatches 343; Indels 157; Gaps 30;

Qy 26 GEVNFSGSKGRKFRVPSVGVAPSVLFDLLAEHLAPNLVSLVSGEQQFAMKSWLR 85
Db 77 GDLDFTYSGRHSNFLRLSDRTDPATVYSLVTRSGFRAPNLVSLVSGSGPVLQTLQ 136

Qy 86 DVLKGLVKAAQSTGAWILTSALRLVGLARHVGQAVRDHSLASTSKRVAVVAGMASLGRV 145
Db 137 DLLRRLGVRAAQSTGAWITVGTGLHTGIGHRVGAVRDHQTASTGSS--KVAVMGVAPWGV 195

Qy 146 LHRRLTEAQRDFFVHY-----PRDDGSGQGLCSLDLSNLSHFILVEPPGPKGDLTEL 200
Db 196 RNRDMLNPKSGFPARYRWGDEP--GVFEP--LDVNSAFFLVDDGTGRLGGENRF 250

Qy 201 RLRLKHLISEORAGYGGTSGIEIPVCLLVNGDPNTERISRAVQOAPWLILVSGGIA 260
Db 251 RLRFPSYVAQKTGVGGTG-IDIPVLLLLIDGDERMLKRIEDATQALPCLLVAGSGAA 309

Qy 261 DVLAALVNQPHLLVP-----KVAEKQFKEKPSKSHSWEDIVRWTKLLQNTSHQHL 313
Db 310 DCLVETLED--TLAPSGGLRRGEARDIRRFPPK-----GDPEVLQAOVERIMTRKELL 362

Qy 314 TVYDFEQRSGSELDIVILKALVKACKSHSQPDYLDLKLAVADRWVDIAKSHIFNGDV 373
Db 363 TVYSSE-DGSEEFETIVILKALVKAC--GSSEASAVLDELRLAVANRWVDIAQSEIFRGI 419

Qy 374 EWKSCDLEVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYSRVSRLKLLFDLQ 433
Db 420 QWRSHLEASLMDALLNDRPEFVRLLIHGLSLGHFLTPVRLAQLYSAVSPNSLIRNLLD 479

Qy 434 RKQEARLITLAGLGTQOAREPPAG-----PPAFSLHESVRLVKDFLODACRGFY----- 482
Db 480 QASH-----ASSSKSPVNGTVELRPP-----NVGQVRLTLTGLTCAPRYPARNT 524

Qy 483 -----QDGRPGDRRAEKGPAPKPTQKWLDDLNQK-----SENWRDLFWAVLQ 528
Db 525 RDSYLQGDHREND-----SLMDMANKQSPSTASFEQAPWSDLLIWAALL 569

Qy 529 NRHEMATYFWAMQEGVAAALAAACKILKEMSHLETAEAARATREA--AKYERLALDLPSE 586
Db 570 NQAQWAIYFWEGKSNVSASALGACLLRLVWARLESEAEAEARRKDLAATFESVDFLFG 629

Qy 587 CYSNSEARAFALLVRRNRCWKTTCILHATEADAKAFFAHGVOAFLTRIMWGDMAAGTP 646
Db 1173 KVLEREVQCSRVLGWVAEALSRSALIPPGGP 1204

Db 630 CYHNSERAARLLRRCLPWGEATCLQAMQADARAFPAQGVQSLLTQKWMGMDSTTP 689
 QY 647 ILRLGALCPALVYNTLTF--SEAPRTGLDQLDLSLDTKSPGLYQGVSEELV 704
 Db 690 IYALLAFPCPLLYTNLIVFRKSEETQKOLD--FDMDSINGAGPGGIVESAVAL 747
 QY 705 EAPRAGDGRPRAVF--LLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPP 761
 Db 748 E--RRQRPRGALCCGFKSKWSDFWGAPVTAFLGNVVSLLFLLLFAHVLVDFQPTK 805
 QY 762 QGSPSEVTLVYVWTVLVEIRQGF-----FTDEDTHLVKKFTLYVGDNNKC 810
 Db 806 --PSVSELLYFWAFTLLCELRQGLGGWGLASGGGRPDRAPLRHLHLVLSDTWQC 863
 QY 811 DNVAIFLFLVGVTCMLPSAFEGRTVLAMDPMVFTLRLHI FAIHKQLGPKIIVVERMM 870
 Db 864 DLLATCTLLGVGCLTGLDGRVLCDFMTFTLLHIFTVNNQLGPKIVSVSKM 923
 QY 871 KDVFLLFLSVLVAVGVTTQALLHPHDGRLEWIFRVLRYPLQIFGQIPLDIDEAR 930
 Db 924 KDVFLLFLSVLVAVGVATEGILRPQDRSLPSILARVYRPLQIFQIPQEMDVAL 983
 QY 931 V---NCS-----THELLEDSP---SCPSLYANWLIVLLVTVLTVNLLNLIAMF 978
 Db 984 MIPGNCSEWERSWHP-----EGPVAGSCVQYANWLVLVLLVFLVANILLNLIAMF 1039
 QY 979 SYTFQVQGNADMFQPKQRYNLIVYHERPALAPPFTLLSHLSLTLR-----RVFKK 1030
 Db 1040 SYTFKVGNSDLYKWAQRYSLIREFHSRPAAPPILIIHVRLIIKWLRCRCRAWL 1099
 QY 1031 EAEKREHLERDLPDLDQKVTVTWQENFUSKWKERRRDSGEVRLKTAHRVDFIAK 1090
 Db 1100 PASPVFHFVCLSKAEARLLTWESVHKENFLLAQARDKSDSRLKRTSKQVDTALK 1159
 QY 1091 YLGLREQEKRICKLESQINQSVLVSSVADVLAQGGPRSQHCGEGSQLVAADHRGL 1150
 Db 1160 QLQGIREVDRRLGLEREVCHSRVITWAEALSH-----SALL----- 1198
 QY 1151 DGWEQPCAGOPPSDT 1165
 Db 1199 -----PPGAPPPSPSPT 1209

RESULT 11
 Q96L84
 ID Q96L84 PRELIMINARY; PRT; 1040 AA.
 AC Q96L84;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE TRP-related cation influx channel (Transient receptor potential cation channel subfamily M member 4 splice variant A).
 GN Name=TRPM4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21438010; PubMed=11535825; DOI=10.1073/pnas.191360198;
 RA Xu X.-Z., Moebius F., Gill D.L., Montell C.;
 RT "Regulation of melastatin, a TRP-related protein, through interaction with a cytoplasmic isoform";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:10692-10697 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Xu X.-Z., Moebius F., Gill D.L., Montell C.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
 RA Hofmann T., Chubakov V., Gudermann T., Montell C.;
 RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent

selective cation channel.";
 RT Curr. Biol. 13:1153-1158 (2003).
 DR EMBL; AY046396; AAL02142.1; -
 DR EMBL; AY297044; AAP44473.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0004872; P:receptor activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002111; Cat_channel_Trlp.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Ion_trans; 1.
 KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
 SQ SEQUENCE 1040 AA; 115564 MW; 684A8C554B2B0F2E CRC64;

Query Match 35.9%; Score 2184.5; DB 2; Length 1040;
 Best Local Similarity 45.3%; Pred. No. 3.5e-137;
 Matches 486; Conservative 156; Mismatches 320; Indels 111; Gaps 26;

QY 125 LASTSTKRVVAVGMSLGRVLRHRLLEEAQEPFVHY-----PEDDGGSGQLCSLDSN 179
 Db 1 MASTG-GTKVAVGVAVGVVVRNRTLINPKGFPARYWRGDPD--GVQFP--LDYN 54
 QY 180 LSHFLLVPEPGPKGDLTBLRLRLEKHISEQAGYGGTGSIBIPVLCILVNGDPMTLER 239
 Db 55 YSAFFLVDDGTHGCLGENRFRRLRESYISQQTGVGGTG-IDIPVLLLLIDGDEKMLTR 113
 QY 240 ISRAVEQAAPWLILVSGGGIADVLALVNQPHLLV-----KVAKQFKEKFPKSHFS 292
 Db 114 IENATQALPCLLVAGSGGADCLAELED--TLAPGGCGARQGEARDIRFFPK-- 167
 QY 293 WEDIVWTKLLQNTSHQHLTVDFEQRSGSELDITVLKLVKACKSHSQSDQYLDL 352
 Db 168 -GDEVLQAVRIMTRKELLTVYSSE-DGSEEFETVLKLVKAC--GSSEASAYLDEL 223
 QY 353 KLAVANDRVDIKSEIFNGDVKNKCDLEVMVDALVNKNPEFVRLFVNDGADVADFLTY 412
 Db 224 RLAVANRVDIKSEIFNGDVKNKCDLEVMVDALVNKNPEFVRLFVNDGADVADFLTY 283
 QY 413 GRLOELYSRVSRSKLLFDLLQKQBEARLTLAGL--GTQOAREPPAGPAPSLHEVSEVL 470
 Db 284 MRLAQLYSAAPNSLIRNLLDQASHAGTKAPALKGGAAELRPP-----DVGHVL 333
 QY 471 KDFLODAGCFYDGPDRRAEKGPAKRPFGKWLDDLNQK-----ENPRDL 521
 Db 334 RMLLGKMCAPYPSGGAWDPH-----PQGGESNYLLSDKATPSLSDAGLQAPMSDL 388
 QY 522 FLWAVLONRHENATYFWAMGQGVAAALAAACKILKEMSHLETEAARATREA--KYERL 579
 Db 389 LLWALLLNRAQMAMFWEMGSNAVSSALGACILLRVMARLEPDAAEARRDLAPKEGM 448
 QY 580 ALDLESECYSNSEAPAFALIVRRNRCSKTTCLHLATEADAKAFHAGDGVQAFTRIWWG 639
 Db 449 GVDLGECTRSRSEVRAARLLRRCPLMGDATCLQAMQADARAPFAQGVQSLLTQKWMG 508
 QY 640 DMAAGTPIRLILGALPCPALVYTNLTF--SEAPRTGLDQLDLSLDTKSPGLYGLQ 697
 Db 509 DWASTTPIWALVLAFFCFPLIYTLIIFRKSSEEPTRREE--FDMDSVINGPGVGTAD 566
 QY 698 SRVLEVEAPRAQGD-----RGPRAVFLTLTRKFWGAPVTVFLGNVVMYFAFLFLF 749
 Db 567 PAEKITPLGVPRQSGRPGCCGRCRRC---LRWFHFWGAPVTFMGNVVSLLFLFLF 623
 QY 750 TYVLLVDFRPPPPQSGPEVTVLFWFTLVLEIRQGFDTDET-----HLVKK 798
 Db 624 SRVLLVDFQAP--PGSLELLYFWAFTLLCELRQGLSGGSGLASGGPGFGHLSOR 681
 QY 799 FTLVYGNWNKCDMVAIFLIVGVTICMLPSAFEGRTVLAMDPMVFTLRLHI FAIHKQ 858
 Db 682 LRLYLADSNWQCDLVALTCPLLGVCRLTGLVHLGRTVLCIDFMVFTVLLHIFTVNNQ 741
 QY 859 LGPKIIVVERMMKDVFFFLFFLSVLVAVGVTTQALLHPHDGRLEWIFRVLRYPLQIF 918
 Db 742 LGPKIIVVERMMKDVFFFLFFLSVLVAVGVATEGILRLPRDSDPFPFSLRVRVRYPLQIF 801

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QY 919 GOIPLEIDEARV---NCSTHPLLEDSP-----SCPSLYANWLVILLVTFLLVTVNVL 970
DB 802 GOIQEDMDVAMEHNSCSSEPGFWAHPGQAAGTCVSOYANWLVILLVTFLLVTVNVL 861
QY 971 NLLIAMFSYTFQVVGQNMDFKQRYNLIYVHERPALAPPFILLSHLSLTIRRVFKK 1030
DB 862 VNLIIAMFSYTFGKVGQNSDLYWKAQRYLRIREFHSRPAAPPFIVISHLRLQLCR 921
QY 1031 -----EAPHKEHLERDLPDLDOKVVTWQENFLSKWEKRRDSEGEVLKRT 1081
DB 922 PRSPQSSPALEHFRVYLSKE-----AERKLLTWESVHKENFLARADKRESDSLKRT 977
QY 1082 AHRVDVFIKYLGLLEGEQKRIKLESQINYSVSVADVLAQ-----GSP 1129
DB 978 SOKVDLALKQLGHIREYEQRLKVLEREVOQCSRVLGWVAEALSRSALLPPGPF 1030

RESULT 12
Q9NXV1 PRELIMINARY; PRT; 1016 AA.
AC Q9NXV1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ20041.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Kawabata A., Hikiji T., Kobatake N., Inegaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obyashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isoqai T., Sugano S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000048; BAA90907.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion trans; 1.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW ION TRANSPORT; IONIC CHANNEL; TRANSMEMBRANE; TRANSPORT.
SQ SEQUENCE 1016 AA; 113245 MW; F640689A3D94DC6D CRC64;

Query Match 35.5%; Score 2164; DB 2; Length 1016;
Best Local Similarity 45.6%; Pred. No. 8.1e-136;
Matches 480; Conservative 150; Mismatches 316; Indels 106; Gaps 25;

QY 125 LASTSTKRVVAVGMASLGRVLRHRLLEAEQDFVHY-----PEDGSGQGPLCSLDSN 179
DB 1 MASTG-GTKVAVGAPWGVNRDRLINPKGSFPARYRWGDPED--GVQFP---LDYN 54
QY 180 LSHFIVGPPGKDGCLTELRLRLKHSIQAGYGGTSGEIPVLCILVNGDPNLTIR 239
DB 55 YSAFFLVDDGTHCGGGRFRRLRLSYISQKTVGGTG-IDIPVLLLLIDGDERKMLTR 113
QY 240 ISRAVEQAAPWLLVSGGGIADVLAVNQPHLLVP-----KVAEKQFKKFPKSKHFS 292
DB 114 IENATQAPCLLVAGSGGAUCLAEITLED--TLAPSGGARQGEARDRIRFFPK----- 167
QY 293 WEDIVRWTKLLQNITSHQHLITVYDFEQEGSEELDTVILKALVKACKSHSQEPQDYDEL 352
DB 168 -GDLEVLQAQVERIMTRKELLTVYSSE-DGSEEFETIVLKALVKAC--GSSEASAYLDEL 223
QY 353 KLVAVNRVDIAKSEIFNGDVEWKSCDLEWMDALVSNKPEFVRLPVDNGADVADFLTY 412
DB 224 RLAVAVNRVDIAQSEIFRGDIQWRSFHLEASLMDALLNDRLPFEFVRLISHGLSLGHFLTP 283
QY 413 GRLOELYRSVRSKLLPDLQKQEEARLTLAGI--GTQQAEREPPAPGPAFSLHSEYRVL 470

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DB 284 MRLAQLYSAAPSLSLRNLLDQASHSAGTAPKAPLKGGAELRPP-----DVGHVL 333
QY 471 KDFLDQACRFYQDGRPGDRRAEKGPAPKPTQKWLLDLNQKS-----ENPRDL 521
DB 334 RMLLGKWCAPRYPSGGAWDPH-----PGQGFGEWYLLSDKATSPSLDAGLQAPWSDL 388
QY 522 FLNAVLRNHEMATYFWAMQOEGVAAALAAACKILKENSHELETEAARATREA--KYERL 579
DB 389 LLWALLNRAQMAWYFWEMGNSNAVSSALGACLLRLVRVARLEPDAEAAARRKDLAFKPEGM 448
QY 580 ALDLPFSCYNSSEARAFALLVRNRNCWSKTCIHLATEADAKAPFAHFDGVOAFTRTWG 639
DB 449 GVDLFGECYRSESVRAARLLRRCPLMGDATCLQAMQADARAFQAQGVQSLITQKWWG 508
QY 640 DMAAGTPIRLILGAFALCPALVYTNLITF--SEEAPLRTGLDLDQDLSLDTKESPLVQLQ 697
DB 509 DMASTPIWALVLAFFCPPIIYTRLIITFRKSEBETREELE--FDMDSVINGECPVGTD 566
QY 698 SRVEELVEAPRAQD-----RGPRAVFLLTWKFWGAPVTVFLGNVVMYFAFLFLF 749
DB 567 PAEKTPLGVPRQSGRPGCGGRCGRRC---LREWFHFWGAPVTTFMGNVVSYLLFLLLF 623
QY 750 TYVLLVDFRPPPGSGPEVTLVFWFVTLVEEIRQGFETDEDT-----HLVKK 798
DB 624 SRVLLVDFQAPAP--PGSLELLLYFWAFTLLCEEURLQGLSGGGSLASGPGPGPHASLSQR 681
QY 799 FTLVVGDNWKNKDMVAIFLFIYGVTCRMLPSAFAGRTVLAMDPMVFTLRLIHIPAIHKQ 858
DB 682 LRLVLAWSNQCDLVALTCFLLVGCRITPGLYHLGRVLCIDFMVFTVRLHLHIFTVNQ 741
QY 859 LGPKIIVVERVMKDVFFFLFPLSVLVWVAYGVTQALLPHPHGRLEWIFRRVLYRYLQIF 918
DB 742 LGPKIIVSVKMKDVFFFLFPLSVLVWVAYGVTQALLPHPHGRLEWIFRRVLYRYLQIF 801
QY 919 GOIPLEIDEARV---NCSTHPLLEDSP-----SCPSLYANWLVILLVTFLLVTVNVL 970
DB 802 GOIQEDMDVAMEHNSCSSEPGFWAHPGQAAGTCVSOYANWLVILLVTFLLVTVNVL 861
QY 971 NLLIAMFSYTFQVVGQNMDFKQRYNLIYVHERPALAPPFILLSHLSLTIRRVFKK 1030
DB 862 VNLIIAMFSYTFGKVGQNSDLYWKAQRYLRIREFHSRPAAPPFIVISHLRLQLCR 921
QY 1031 -----EAPHKEHLERDLPDLDOKVVTWQENFLSKWEKRRDSEGEVLKRT 1081
DB 922 PRSPQSSPALEHFRVYLSKE-----AERKLLTWESVHKENFLARADKRESDSLERT 977
QY 1082 AHRVDVFIKYLGLLEGEQKRIKLESQINYS 1113
DB 978 SOKVDLALKQLGHIREYEQRLKVLEREVOQCS 1009

RESULT 13
Q7Z5D9 PRELIMINARY; PRT; 1069 AA.
AC Q7Z5D9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transient receptor potential cation channel subfamily M member 4 splice variant C.
GN Name=TRPM4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
RA Hofmann T., Chubakov V., Gudermann T., Montell C.;
RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent selective cation channel."
RL Curr. Biol. 13:1153-1158(2003).
RL EMBL; AY297046; AAP44475.1; -.

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RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK044094; BAC31771.1; -;
DR MGD; MGI:1915917; Trpm4.
DR GO; GO:0016021; C.integral to membrane; TAS.
DR GO; GO:0005886; C.plasma membrane; IDA.
DR GO; GO:0005262; F.calcium channel activity; IDA.
DR GO; GO:0006816; P.calcium ion transport; IDA.
DR InterPro; IPR002111; Cat channel_Trlp.
DR InterPro; IPR005821; Ion trans.
DR Pfam; PF00520; Ion trans_1.
DR Ion transport; Ion channel; Transmembrane; Transport.
RW Ion transport; Ion channel; Transmembrane; Transport.
SQ SEQUENCE 945 AA; 105526 MW; B7261C0A368666EB CRC64;

Query Match 34.0%; Score 2069; DB 2; Length 945;
Best Local Similarity 45.8%; Pred. No. 1.7e-129;
Matches 455; Conservative 141; Mismatches 124; Gaps 27;

QY 100 GAWILTSALRVGLRHVGQVRDHSLASTSTKRVVAVGMSLGRVLRHRIIEAQEDPP 159
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4 GAWIVTGGTGTGIRHVGVAVRDQSTGSS-KVAVMGVAPMGVVRNDRMLNPKGSFP 62
QY 160 VHY-----PEDGSGSQCLSDSNLSHPTLVPEPPGPGDGLTELRLLKHXISQRA 214
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 ARYWRGDPED--GVEFP---LDYNISAFPLVDGTYGRVLRGGRNRRFLRFESVAQK 117
QY 215 YGCTGSTEIPVCLLVNGDPNTLIERISRAVEQAPWLLVVGSGGIADVLAAVNP 274
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 118 VGTG-IDIPVLLLLIDGDEKMKRIEDATQAQLPCLLVAGSGGAACLVETLED--TL 174
QY 275 P-----KVAEQKFKPKSPKSPSWEDIVRWTKLLQNTISHOHLITVYDFEGSEELD 327
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 PGSGGLRRGEARDIRRYFPK-----GDPEVLAQVVERIMTRKELLTVYSSE-DGSE 228
QY 328 TVTLKALVACKSHSOPQDYLDELKLAVDWRVDIAKSIIFNGDVEWKSCLDEEVWVDA 387
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 229 TIVRLALVKAC--GSSASAYLDELRLAVANWRVDIAQSELFEGDQWRSFHLEASLMD 286
QY 388 LVSNKPEFVRLVDNGADVADFTYGRLOELYSRVSRSKSLLPDLQKQBEARLTLAGLG 447
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 287 LINDREFVLLISHGLSHGLFTPVRLAQLYSNVSNLSIRNLDDQASH----- 336
QY 448 TQQAAREPPAG-----PPAFSLHEVSRVSKDFLQDACRGY-----QDGRPGDR 490
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 337 ASSSKSPVNGTVELRPP-----NVGQVRLTLIGETCAPRYPARNTRDSYLGQDHREND- 390
QY 491 RRAEKGPAKPTGQKWLIDLNQK-----SENWEDFLWAVLQNRHEWATYFWAMGQ 542
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 391 -----SLMDWANKQKPTSDASFEQAPWSDLLIALLWLNRAQWALYFWKSGS 436
QY 543 EGVAALAAACKILKEMSHLETAEAARATRE--AKYERLALDLFSECYSNSEARAFALLV 600
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 437 NSVASALGACLLLRVWARLSEAEARRRKDLATFESMSVDLFGECYHNSEERARLLL 496

601 RRNRCSKTTTCLHLATEADAKAFPAHQVQAFPLTRIWMGDMMAAGTPILRLLAGFLCPALV 660
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
497 RRCPLWGEATCLQLAMQADARAFPAQGVQSLLTQKWMGEMDSTTPIWALLAFPCPLI 556
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
661 YTNLITP--SEEAPLRTGLEDLQDLSLDTSEKSPYGLQSRVEELVEAPRAQGDGPRAV 718
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
557 YTNLIVFRKSEETQKDL--FDMSSINGAGPPGTVEPSAKVALE--RRORRRPGRAL 612
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
719 F---LLTRWRKFWGAPVTFLGNVMYFAFLFLTYVLLVDFRPPQSGPSGPEVTLYFWV 775
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
613 CCGFKSKWSDFWGAFTAFNGVSVYLLFLLFAHLLVDFQPTK--PSVSELLLYFWA 670
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
776 FTLVLEIRQGF-----FTDETHLVKFKFTLVVGNWNKCDWVAIFLFIUVGTC 824
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
671 FTLLCEELRQGLGGGWSLASGGRGPDRAPLRHLRLHLYLSDTNQCDLLALTCLFLGVGC 730
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
825 RMLPSAPAGRTVLAMDVMTLRLIHLFAHKQLGPKIIVVERMMKQVFPFLFLSVWL 884
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
731 RLTPGLFDLGRVLCDFMIFTLRLHIFTVKNQKLGPKIVIVSKMKDQVFFFLFLCVWL 790
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
885 VAYGVTTQALLPHDGRLEWIFRRVLYRPYLIQIFQIPLDEIDEARV---NCS-----T 935
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
791 VAYGVATEGILRPQDRSLPSILRRVRYRPYLIQIFQIPEQENDVALMIPGNCSEMERGWA 850
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
936 HPLLLEDSF---SCPSLYANMLVILLVTLVTLVTLVLLNLLLIAMFSYTFQVVGNAFMD 992
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
851 HP----EGPVAGSCVSVQYANMLVLLVLLVLLVANILLNLLLIAMFSYTFKSVHGNSDIY 906
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
993 WKFYQNLIVYHERPALAPPFILLSHLSLTLRR 1026
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
907 WKAQYSLIREFHSRPPALAPPLIIICHVSYSVRK 940

RESULT 15
TRL2 HUMAN
ID TRL2 HUMAN STANDARD; PRT; 1503 AA.
AC O94759; Q96KNG;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Long transient receptor potential channel 2 (LTPC2) (Transient
DE receptor potential channel 7) (TRPC7).
GN Name=TRPM2; Synonyms=KNP3, LTRPC2, TRPC7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99026133; PubMed=9806837; DOI=10.1006/geno.1998.5551;
RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Asakawa S., Ito F.,
RA Shimizu N.;
RT "Molecular cloning of a novel putative Ca2+ channel protein (TRPC7)
RT highly expressed in brain";
RL Genomics 54:124-131(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX PubMed=11960981; DOI=10.1074/jbc.M112096200;
RA Wehage E., Eisfeld J., Heiner I., Jungling E., Zitt C., Luckhoff A.;
RT "Activation of the cation channel long transient receptor potential
RT channel 2 (LTPC2) by hydrogen peroxide. A splice variant reveals a
RT mode of activation independent of ADP-ribose";
RL J. Biol. Chem. 277:23150-23156(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Biechmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,

Db 1137 QFQKQRPQKIEDISNKVDAMVDLDDPLKRSMS--EORLASLEEQVAQTARALHW 1193
Qy 1119 VADVLAQGGPRSSQHCSEGSQVAAD---HRGGLDGWEQPG 1157
Db 1194 IVRTLRSAGFSSEADVPTLASQKAAEEPDAPFGGRKKTEEPG 1235

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